

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 24, 2004, 17:43:31 ; Search time 41 Seconds
(without alignments)
940.800 Million cell updates/sec

Title: US-09-813-718-1C_COPY_71_471

Perfect score: 2116

Sequence: 1 SNHGDATTAEEEDVDPWTV.....VTDBIVXEMTPRKLSPFDEQ 401

Scoring table: BIOSTM62

Gapop 10.0 , Gapext 0.5

Searched:

283366 seqs, 9619:526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

PIR 78:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2101	99.3	471	1 A4106	tryptophanyl-tRNA li
2	2028.5	95.9	475	1 YNHO	tryptophanyl-tRNA li
3	1946.5	92.0	475	1 YNRBPR	tryptophanyl-tRNA li
4	1938	91.6	481	2 S50053	tryptophanyl-tRNA li
5	1210	57.2	395	2 S55157	hypothetical protein
6	1163	55.0	432	2 S51901	tryptophanyl-tRNA li
7	957	42.9	386	2 C30190	tryptophanyl-tRNA
8	803	37.9	385	2 C75020	tryptophanyl-tRNA li
9	626.5	29.6	301	2 G1206	tryptophanyl-tRNA li
10	25.3	25.3	380	2 G84373	tryptophanyl-tRNA li
11	409.5	13.4	370	2 F64476	tryptophanyl-tRNA li
12	397.5	18.8	364	2 B69131	tryptophanyl-tRNA li
13	386	18.3	134	2 T42806	tryptophanyl-tRNA li
14	372.5	17.5	420	2 E69461	tryptophanyl-tRNA
15	353	16.7	374	2 D72477	probable tryptophanyl-tRNA
16	269.5	12.7	513	2 F84371	tryptophanyl-tRNA
17	192	9.1	323	2 H63346	tryptophanyl-tRNA synth
18	188	8.9	364	2 E75512	probable tyrosyl-tRNA
19	185.5	8.8	341	2 D95260	tryptophanyl-tRNA
20	185.5	8.8	341	2 G98125	tryptophanyl-tRNA li
21	174.5	8.2	341	2 B86533	tryptophanyl-tRNA li
22	172	8.1	334	2 A45999	tyrosine-tRNA ligase
23	170.5	8.1	366	2 S75410	tryptophanyl-tRNA
24	169	8.0	395	2 H70385	tryptophanyl-tRNA
25	167	7.9	351	2 E75438	tryptophanyl-tRNA
26	166.5	7.9	346	2 B71496	tryptophanyl-tRNA li
27	164.5	7.8	395	2 A85410	protein F3M8 22 [
28	163.5	7.7	353	2 E70100	tryptophanyl-tRNA
29	163	7.7	460	2 C84500	probable tyrosyl-tRNA

RESULT 1

A41706

tryptophanyl-tRNA ligase (EC 6.1.1.2) [similarity] - human

N: Alternative names: interferon-inducible protein IFP53; peptide-chain release factor homolog

C: Species: Homo sapiens (man)

C: Date: 19-May-2000 #seq=1000 #text change 03-Jun-2002

C: Accession: A41633; A41706; S19246; JNC6716; JH0533; S26287

R:Flechner, J.; Rasmussen, H.H.; Justesen, J.

Proc. Natl. Acad. Sci. U.S.A., 88, 11223-11224, 1991

A: Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma

A: Reference number: A41633; MUID:92107982; PMID:1763065

A: Accession: A41633

A: Status: Preliminary

A: Molecule type: mRNA

A: Residues: 1-471 <FILE>

A: Cross references: GB:X59892; PID:933820; PID:CARA2545.1; PID:g30821

R: Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.

J. Biol. Chem., 266, 24245-24248, 1991

A: Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts

A: Reference number: A41706; MUID:92105071; PMID:153132

A: Accession: A41706

A: Status: Preliminary

A: Molecule type: mRNA

A: Residues: 1-471 <RUB>

A: Cross references: GB:M77804; PID:g1846556; PID:AAA67324.1; PID:g184657

R: Bawitz, U.; Plohr, T.; Boettger, B.C.

EBO J. 11, 489-496, 1992

A: Title: Molecular cloning and characterization of an interferon induced human cDNA with

A: Reference number: S19246; MUID:92144636; PMID:153132

A: Accession: S19246

A: Status: Preliminary

A: Molecule type: mRNA

A: Residues: 1-423, R' <BOW>

A: Cross references: EMBL:X62570; PID:S32708; PID:CAA44450.1; PID:g184657

R: Prokrova, I.Y.; Grigorieva, A.Y.; Sudomina, M.A.; Kisseliev, L.L.

Gene 128, 237-245, 1993

A: Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response element

A: Reference number: JN0676; MUID:7685728

A: Accession: JN0676

A: Molecule type: DNA

A: Residues: 1-141; 182-471 <FR0L>

A: Cross references: GB:X67918; GB:S62837; NID:937968; GB:X67919; NID:937969; GB:X67920; NID:937970

4; NID:937974; GB:X67925; GB:S62855; NID:937975; GB:X67926; GB:X67927; NID:937976; GB:X67928

A: Note: the authors translated the codon GGG for residue 55 as Cys and GAG for residue 34

A: Note: this translation is not annotated in GenBank entries HSWRSX1, HSWRSX2, HSWRSX2

R: Prokrova, I.Y.; Sudomina, M.A.; Grigorieva, A.Y.; Kisseliev, L.L.

Gene 109, 219-226, 1991

A: Title: Cloning and nucleotide sequence of the structural gene encoding for human trypto

A: Reference number: JH0533; MUID:92112058; PY:D:1765274

A: Molecule type: mRNA

A: Cross references: EMBL:Y01100; PID:9329992; PID:9329992; PMID:7685728

ALIGNMENTS

A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 C;Species: Pyrococcus abyssi
 C;Accession: C75020
 C;Superfamily: Rianomous, Genoscope submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A;Reference number: A75001
 A;Accession: C75020
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-385 <RAW>
 A;Cross-references: GB:AUJ248288; GB:AL096836; NID:95458960; PIDN:CAB50601.1; PID:9545911
 A;Experimental source: strain Orsay
 A;Gene: trps; PAB111
 C;SuperFamily: mammalian tryptophanyl-tRNA ligase; amino acid-tRNA ligase repeat homology

Db	346	IDKUNNFLEBR-RERBEAKELVHVERYDERRKA	377	
RESULT 8				
C;Species: Pyrococcus abyssi				
C;Accession: C75020				
R;ianomous, Genoscope submitted to the EMBL Data Library, July 1999				
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure				
A;Reference number: A75001				
A;Accession: C75020				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-385 <RAW>				
A;Cross-references: GB:AUJ248288; GB:AL096836; NID:95458960; PIDN:CAB50601.1; PID:9545911				
A;Experimental source: strain Orsay				
A;Gene: trps; PAB111				
C;SuperFamily: mammalian tryptophanyl-tRNA ligase; amino acid-tRNA ligase repeat homology				
Query Match	29.6%	Score 62.5;	DB 2;	Length 301;
Best Local Similarity	44.2%	Pred. No. 1-8e-42;	Indels 21;	Gaps 7;
Matches 134;	Conservative	56;	Mismatches	
Qy	99	MAVGHUPEPITFKWLQDENVPLVINTDCKLND-LTLDQAYDAVENAKRDIIAGCF 157		
Db	1	MAIGHIIPPFATWKWLQKFQGVNLYIQTTDEKFLENLTEDDT-KRKAQNLDIATWGF 60		
Qy	158	DINKTFISLDYMGMSGFYKNWVK-QKHYTENQVKIGFTESD-LIGKTSFPAIQAP 217		
Db	61	DEDKTFIFQNSEF---TKIVEMAIPFLAKKINFMSAKAVFGFTEQSXIGMFFPAIQAP 116		
Qy	218	SFSNSPFPQIQRDRTDIQCILPACIADDPYPRMTDVAPARIGYPKPALLESTFPALOGAQ 277		
Db	117	TF-----FPERK---RCILPAIAQDPYWRQDPAESLGQYKTAHALSKSKEVPSLTLS 166		
Qy	278	TMSASDPNSNISFLTTQKQITKQHAFSGQDRTIEBHQGKQHAFSGQDRTIEBHQGKQHAFSGQDVSFMYLTFL 337		
Db	167	GMMSASKPETAQYLDSPEDEVKWKFTEGGRPLIKEQREKGGEPEKCVUFKWLFFF 226		
Qy	338	EDDKLEQIRKDY---TSGAMLTGELRKKALTEVLQPLIAEHDQARRKEYTDELVEKFPMTPR 394		
Db	227	BEDDK--KLKERRYACKNGEILTGCBECKRYLISKIQEFLIKEHORRKK-AEKLVKEFKYTG 283		
Qy	395	KLS 397		
Db	284	KLA 286		
RESULT 10				
Qy	59	RDYDKVQLQDYEGRGFFLYTGRGPSSBEMHVGHLSPFIFKWLQDQVNFVPLVINTQDDEK 130		
Db	131	YLWD-LTLDQAYDAVENAKRDIIAGCDFDINKTFLISLDYMGMSGGFYKNWVK-QKHYT 189		
Qy	118	FLPENLTFEDTRHAYENLIDLIAVGDFEPKTFIQNSEF---TKIVEMAIPARKIN 173		
Db	190	ENQYKIGIEFTSDCIGKISFPQIAQAPSFSNSFFPQIERTDRTQCLIPCAIDDPYFRM 249		
Qy	174	FSMAKAEGTEQSKMGPATIQLAPT----FEKR---RCLIPAAIDQDQEYWRL 223		
Db	250	TRYDAPRIGPKPALHSTPPALQQTQTMASDNPNSSTPLTDQKIKTKWKGAFSG 309		
Qy	224	QRDFAESLGLYKTAIHSKVEPLTSLSGKMSASKPETAQYLTDSPDVEKKWKFPLALTG 283		
Db	310	GRDTLEBHFQFGNCDVDSEMFYMLTFEDDK-EQIRKDY---TSGAMLTGELRKALIE 366		
Qy	284	GPFLIKEQFRKGKGFPEKCVWFKWLQFEEBDK-KLKERRYACRNGETGECRYLIS 341		
Db	367	VLOPLIAEHQARRKEYTDELVK 388		
Qy	342	KIQEFLIKEHQRKRAEKQIEK 363		
RESULT 9				
C;Species: Pyrococcus horikoshii				
C;Accession: G71206				
R;ikawa-horikoshi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekirin M.; Ofukita, T.; Funabashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi DNA Res. 5, 55-76, 1998				
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon: G71206				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-301 <RAW>				
A;Cross-references: GB:AP000007; NID:93236134; PID:BA31046.1; PID:9325833				
Query Match	25.3%	Score 53.4;	DB 2;	Length 380;
Best Local Similarity	35.4%	Pred. No. 8e-36;	Indels 41;	Gaps 17;
Matches 141;	Conservative	76;	Mismatches	
Qy	10	AEEDFDVPTWQTSSAKGKDYDGLIREGSSKIDKELINRLERATSORPHFLRQFIES 69		
Db	3	ADGNDTPTVATESDD---LDYEQKLJLARGADELTQDQRARP----DHP-LNRRGFLYA 53		
Qy	70	HRDMQVLDAYENKKEFYLYTGRGPSEAMEVGHLTIFPKWLDQDVENVJNQIMDE 129		
Db	54	GRDVFDFLTAEHQCS---TIVQVGPSC-PHEGLAHMVYFARRQEVGARYVPPSDE 108		
Qy	130	KYLWD-LTLDQAYDAVENAKRDIIAGCDFDINKTFL---SDLDXN-GMSSGEYKNNVKZ 184		
Db	109	KYWFQDQTPAET-GDYLRAANDLAVGFDPELTVVVDERJDADLYPLATAFAGJV--- 164		

QY	^85 QKHTVTFNQVKGIGFTDSDCIGKISPAIQAAAPSFSNSPPIFRDRTDIOCLIPCAIDQD 244	Db	340 AYERWVFQKOLIKEKREJAKEATAVK 364
Db	165 -RHATIONVIG----EPDNNGQAAFPVQTAELL---LPQLMHG--EHETLVPIAODQD 213		RESULT 12
Qy	245 PYFRMTRDVAPIGYP--KPAUHSTFPPALOGAQATKMSASDPNSSTFLDTAKQIKTKV 302		B69131
Db	214 PHVRVERDVAARAKARYPGKPGALLMQP--PSLAG-PGRMSASAGVSARLTDPSDTREKV 271		tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Delta C)
Qy	303 NKHAFASSGRDITIEHROFGGNCDVDSFMYLTFLIEDDD-KLEQIRKDYTSGAMLTCELK 361		tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum (strain Delta C)
Qy	272 RTHAYTSGRASVEEHRAKGGVPAEDWFOQLSAFFPDAELARIEREYRAGSDLLSCELK 331		#sequence_revision 03-Dec-1997 #text_change 03-Jun-2002
Db	362 KALLEVQPLIAHQARRKEVTDIYKFMTDRKLSED 399	C;Species: Methanobacterium thermoautotrophicum	R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.J. E
Qy	332 DLAADRTEFLAAHQRRRAALGD--VTEALDAFRLTDD 367	C;Keywords: Methanobacterium thermoautotrophicum	i Qiu, D.; Spadaiora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noellring, J.; Reeve, J.N.
Db		A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct:	J. Bacteriol. 179, 7135-7155, 1997
		A;Reference number: A69000; MUID:98037514; PMID:9317463	A;Accession: B69131
		A;Status: preliminary; nucleic acid sequence not shown; translation not shown	A;Molecule type: DNA
		A;Residues: 1-364 <WTH>	A;Cross-references: GB:AE000812; GB:AE000666; NID:92621298; PIDN:AA884757.1; PMID:92621301
		A;Experimental source: strain Delta H	A;Genetics:
		C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology	C;Genetics:
		C;Accession: MT2511	A;Start codon: TTG
		C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis	C;Superfamily: mammalian tryptophan-tRNA synthetase; ligase; protein biosynthesis
		Qy	Query Match 16.8%; Score 397.5; DB 2; Length 364;
		Db	Best Local Similarity 27.9%; Pred. No. 1..le-24;
		Qy	Matches 107; Conservative 76; Mismatches 153; Indels 47; Gaps 14;
		Db	15 VDPWTWVTSAGTIDYDKLIVTRFGSSSKIDKEINRTRATGPYPHFLRGRGFFSHDMN 74
		Qy	2 IDEW---GSKA-LETQDLIENFGVRPF-SEVDEV---PEPSWMLRGTGFGRDYB 56
		Db	75 QVLDAYENKPKFYLTYGRGPSSSEAHVGHILIPIFTWLDQDENVPLVQIOMTDDEKVINK 134
		Qy	51 RIISMKKGGECAVVTMMPGCR-MHIGKMIVDQLR-N-YDNGAEFTPIADMEAYSAR 108
		Db	135 DLTDQAYGAVEN-AKDIATAGFDINK-----TFLPSDDLMGMSSGFYKNVVK 183
		Qy	109 GVDFFEDSRRLAEEYTAGYIALGLDEKDNT-HHYLQSENLYMEDLATV----- 156
		Db	184 GYKPKALLHSTFFFALOGAQATKMSASDPNSSTFLDTAKQIK 299
		Qy	157 LAGKUNNENLRLAYIYGFTGSTSMAHMYAPIQYSDLHQPDELGGPR -PUTVPVGPD 213
		Db	244 DPYFRMTRDVAPRI---GYPKPALLHSTFFFALOGAQATKMSASDPNSSTFLDTAKQIK 299
		Qy	214 DPHLTRDIAFRDYYGFLPSSTYHRFMGLTG---KESNSNPXPKGAFISDTPPEA 271
		Db	300 TKYKCHFSGRDTIEHROFGGNCDVYSMFLYTFLE-DDEKLEQIORKYOTSGAMLTG 358
		Qy	272 AXI-RNAKTTGRETILEQRELGGPPECIVTELZHMGSRSRLEYESCRNGTLMCG 330
		Db	359 EKKALLEVLQQLIAEEQARRKE 381
		Qy	331 ECKNTAAEPKKEFEELSVKREK 353
		Db	RESULTS 13
		T43806	
		250 TRDVAPR---IGYKPKALLHSTFPAIQLQATKMSASDPNSSTFLDTAKQIKTKVKA 306	tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment)
		225 TRDIANRAKEFKFIPPSSTYHRMTGIGG--KMSSSKPETAFLDTDEKTVKKIFS-A 281	C;Species: Encephalitozoon cuniculi
		307 FSGGRDITIEHROFGG--NCDDYDVSTXYLTFLEDDKLEQIORKYOTSGAMLTGELKKA 363	C;Accession: T43806
		282 KTGIRETLEEHKGGYTYPECTVYELSLY-HLILDDKELASITYQCRSGEFTGCRKMM 339	R;Peyretailade, E.; Broussolle, V.; Peyret, P.; Metenier, G.; Gouy, M.; Virelizier, C.P.
		364 LIEVLOPLIAHQARRKEVTDIYK 388	A;Title: Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene
			A;Reference number: 222691; MUID:98277683; PMID:9615449
			A;Accession: T43806
			A;Status: preliminary; translated from GB/EMBL/DDJB

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2101	SYW_HUMAN	SYW_HUMAN	471	1	P23381	homo sapien
2	2028	SYW_BOVIN	SYW_BOVIN	475	1	P17248	bos taurus
3	1961	SYW_RABBIT	SYW_RABBIT	475	1	P23612	oryctolagus cuniculus
4	1938	SYW_MOUSE	SYW_MOUSE	481	1	P32921	mus musculus
5	1210	SYW_SCHPO	SYW_SCHPO	572	1	Q09692	schizosaccharomyces pombe
6	1163	SYW_YEAST	SYW_YEAST	550	1	Q12109	saccharomyces cerevisiae
7	910	SYW_SULTO	SYW_SULTO	432	1	Q976m1	sulfobolus sulfobolus
8	909	SYW_SULFO	SYW_SULFO	422	8	Q972x0	sulfobolus sulfobolus
9	826	SYW_PYRFU	SYW_PYRFU	385	1	Q8u5y1	pyrococcus pyroccocus
10	803	SYW_PYRAB	SYW_PYRAB	379	9	Q9y5y4	pyrococcus pyroccocus
11	796	SYW_PYRHO	SYW_PYRHO	376	6	Q8ztu5	pyrobaculum
12	735	SYW_PYRAE	SYW_PYRAE	347	7	Q9hn66	halobacteri
13	534	SYW_HAUNI	SYW_HAUNI	253	3	Q9tYf7	metanopyrus
14	453	SYW_MEINKA	SYW_MEINKA	214	1	Q58810	methanococcus
15	409	SYW_METOA	SYW_METOA	194	7	Q26352	methanobacter
16	397	SYW_METH	SYW_METH	188	5	Q9h7y8	thermoplasm
17	386	SYW_ENCCU	SYW_ENCCU	186	1	Q9h7y1	encephalitozoon
18	370	SYW_ARCPU	SYW_ARCPU	175	2	Q28579	archaeodictyon
19	353	SYW_AERPE	SYW_AERPE	167	1	Q9y924	aeropyrum
20	329	SYW_METAC	SYW_METAC	156	1	Q8tpw5	methanosaer
21	313	SYW_METMA	SYW_METMA	148	1	Q978y8	thermoplasm
22	299	SYW_THEVO	SYW_THEVO	142	1	Q9h83	halobacteri
23	269	SYW_HALINI	SYW_HALINI	127	1	Q9h1ws	thermoplasm
24	268	SYW_THEAC	SYW_THEAC	127	1	Q8e2j5	streptococcus
25	203	SYW_STRA3	SYW_STRA3	96	1	Q8dwp7	streptococcus
26	192	SYW_ARCPU	SYW_ARCPU	96	1	Q29482	archaeoglob
27	185	SYW_STRPN	SYW_STRPN	91	1	Q97n42	streptococc
28	185	SYW_STRP3	SYW_STRP3	86	1	Q8n7y2	streptococc
29	183	SYW_STRPY	SYW_STRPY	87	1	Q99xh4	streptococc
30	182	SYW_STRMU	SYW_STRMU	86	1	Q8drri1	streptococc
31	175	SYW_CLOCO	SYW_CLOCO	83	1	Q46127	clostridium
32	175	SYW_LACHLA	SYW_LACHLA	83	1	Q9cd1	lactococcus

C2	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
C3	Mammalia; Batheria; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC	Bovinae; Bovidae.
OX	NCBI_TaxID=9913;
RN	[1] TISSUE->Retina;
RA	RP TISSUE->Retina;
RC	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RE	MEDLINE#91323348; PubMed=1907847;
RA	Gandar J.-C., Payot B., Trezequet V., Labouesse J.-P., Merle M., Gueguen M., Sarger C., Labouesse M.-L., Alterio J., Gueguen M., Sarger C., Labouesse B., Bonnet J.; "A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic synthetases but near identity with mammalian peptide chain release factor"; chain release factor"; [2].
RL	Biochemistry 30:7809-7817(1991).
RN	SEQUENCE OF 17-475 FROM N.A.
RP	TISSUE->France;
RC	Garret M., Trezequet V., Payot B., Gandar J.-C., Merle M., Gueguen M., Bonnet J., Beneffetto J.-P., Sarger C., Alterio J., la Bouessesc B., Submitted (MAR-1990) to the EMBL/GerBank/DBJ databases.
RA	Submitted (MAR-1990) to the EMBL/GerBank/DBJ databases.
RL	-1. CATALYTIC ACTIVITY: ATP + Lryptophan + tRNA(Trp) = AYP + diphosphate + Lryptophanyl-tRNA(Trp).
CC	-1. SUBUNIT: Homodimer.
CC	-1. SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC	CC -1. SIMILARITY: Contains 1 WHEP-TRS domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL: X53918; CAA37872_1; DR: X52113; CAA36356_1; -.
DR	PIR: A0279; YBDB.
DR	InterPro: IPR002305; tRNA-synt_1b.
DR	InterPro: IPR001412; tRNA-synt_I.
DR	InterPro: IPR002306; tRNA-synt_1b.
DR	InterPro: IPR000738; WHEP-TRS.
D2	PFAM: PF00578; tRNA-synt_1b; 1.
D2	Pfam: PF00458; WHEP-TRS; 1.
D2	PRINTS: PRO0339; TRNA-SYNTHTP2.
D2	TIGRFAMs: TIGRF00033; WTPS; 1.
D1	PROSITE: PS003178; AA_tRNA_LIGASE_I; 1.
D1	PROSITE: PS03762; WHEP-TRS; 1.
K1	Aminoacyl-tRNA synthetase: Protein biosynthesis; Ligase; ATP-binding.
F1	DOMAIN 24 69 WHEP-TRS.
F1	DOMAIN 1 117 DISPENSABLE TO THE CATALYTIC ACTIVITY.
F1	SITE 169 "HIGH" REGION.
F1	SITE 353 357 "KMSK" REGION.
F1	CONFLICT 17 17 L -> M (IN REF_2).
S2	SEQUENCE 475 AA; F7E531750137B32 CRC64;
Q1	1 SNIGPDATAEEDFDPWVOTSSAKGIDYDKLTVRGSSSKIDKELINERATGORPHI 60
D1	76 SGIGLDATADEDFDPWVOTSSAKGIDYDKLTVRGSSSKIDKELINERATGORPHI 135
Q1	61 FLRGIFFSHRDMMQVLDAYENKKPFLYLTGRGPSSSEAHUGHLLIPFFKWLQDVNP 120
D1	136 FLRGIFFSHRDMMQVLDAYENKKPFLYLTGRGPSSSEAHUGHLLIPFFKWLQDVNP 195
Q1	121 LVQMTDDEKYLWQDLDLQOAYDAVENAKDIAAGFDINKTFIFSDLDYMGMSGFYKN 180
D1	196 LVQMTDDEKYLWQDLDLQOAYDAVENAKDIAAGFDINKTFIFSDLDYMGMSGFYKN 254
Q1	Query Match Score 208.5; DB 1; Length 475;
Best Local Similarity 95.8%; Pred. No. 1.9e-157;	
Matches 384; Conservative 8; Mismatches 8; Indels 1; Gaps 1;	
DR	EMBL: M33460; AAA31246_1; ALT SEQ.
DR	EMBL: U02595; AAB60357_1; -.
DR	InterPro: IPR002305; tRNA-SYNT_1b.
DR	InterPro: IPR001412; tRNA-SYNT_I.
DR	InterPro: IPR002306; TEP-tRNA-synt_1b.
DR	InterPro: IPR000738; WHEP-TRS.
DR	Pfam: PF00458; tRNA_Synt_1b; 1.
DR	PRINTS: PRO1039; TENASYNTHTRP.
DR	TIGRFAMs: TIGRF00033; TES; 1.
DR	PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.

PROSITE; PS00762; WHEP-TRS; 1.	
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.	
T DOMAIN	23 68 WHEP-TRS.
T SITE	168 177 "HIGH" REGION.
T SITE	353 357 "KMSKS" REGION.
SEQUENCE	475 AA; 537399 MW; 33BC9E718F45DC4 CRC64;
Query Match	92.7%; Score 1961.5; DB 1; Length 475;
Best Local Similarity	91.5%; Bred. No. 5.3e-152;
Matches 367; Conservative 20; Mismatches 13; Indels 1; Gaps 1	
Y 2 NHG-PDATABAREDFDPWTVTQSSAKGIDYDKLIVRPGSSSKIDKEJLNRIERATGQRPHH 60	
Y 75 SHGDPAVDEEDFDPWTVTQSSAKGIDYDKLIVRPGSSSKIDKEJLNRIERATGQRPHR 134	
D 61 FLRRGGFFSHRDMDNQVLDAYENKKPFVLYTRGPSSBAMVGHLLIPITFKMLQDVENVVP 120	
D 135 FLRRGGFFSHRDMDNQVLDAYENKKPFVLYTRGPSSBAMVGHLLIPITFKMLQDVENVVP 194	
I 121 LVQTQDDEXYLWQLDLTQAYGDAVENAKDIIACGFDINKTFPSDIDYMGMSGSFYKN 180	
D 195 LVVQNSDDEKYLWQLDLTQEYQGYTLENDKATIACGFDVKNTFIFSDLDYMGMSGSFYKN 254	
V 181 VVKIGKQHTEFNQVKGSEFGFTSDCIGKISFPAIQAPSFNSFQPIFRDRTDQCLJCPA 240	
D 255 VVKIGKQHTEFNQVKGSEFGFTSDCIGKISFPAIQAPSFNSFQPIFHGQQAIDTQCLJCPA 314	
C 241 IDQDQYFMRTRDVAPIRGYPKPALLISTFPALQGACTKMEASDPNSNISFLDTDAKQIKT 303	
D 315 IDQDQYFMRTRDVAPIRGYPKPALLISTFPALQGACTKMEASDPNSNISFLDTDAKQIKT 374	
P 301 KVNGKAFAFSGRDITIEERQFGNCODVSVSMYLTFLEDDKLEQIRKDQYTSGAMLTGEL 360	
D 375 KVNGKAFAFSGRDITIEERQFGNCODVSVSMYLTFLEDDKLEQIRKDQYTSGAMLTGEL 434	
S 361 KKA11EVQPLIAEHQARRKVTDELYKEWMPK-SSEDFQ 401	
A 435 KRE11DVLQPLVRAEHQARRKVTDELYKEWMPK-SSEDFQ 475	
RESULT 4	
SYN MOUSE	STANDARD ; PRT ; 481 AA.
P335921; 01-OCT-1993 (Rel. 27, Created)	
01-OCT-1993 (Rel. 27, Last sequence update)	
28-FEB-2003 (Rel. 41, Last annotation update)	
TRYPTophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase) (TTRS).	
Mus musculus (Mouse).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10990; [1]	
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).	
MEDLINE-950118226; PubMed-7932716;	
Pajot B., Sanger C., Bonnet J., Garret M.;	
"An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase in murine embryonic stem cells."	
J. Mol. Biol. 242:599-603 (1994).	
- - CATALYTIC ACTIVITY : ATP + L-tryptophan + tRNA _{Trp} = AMP + diphosphate + L-tryptophanyl-tRNA _{Trp} .	
- - SUBUNIT: Homodimer (By similarity).	
- - ALTERNATIVE PRODUCTS:	
Event=Alternative splicing; Named isoforms=2;	
Name=1; Synonyms=long;	
Isoid=P2921-1; Sequence-Displayed;	
Name=2; Synonyms=Short;	
Isoid=P2921-2; Sequence=VSP_006313;	
- - TISSUE SPECIFICITY: Isoform 2 is widely expressed, isoform 1 is found only in embryonic stem cells.	
- - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.	

Putative tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophanyl-tRNA ligase) (TRPS1).

DE	GN	SPACF7_13C.	Oy	67	FESERDMMQVQDAYENKEKPEFLYLTGRGGSSSEKAMHIGLTIPETFLKODVENVILIVQT	126
OS	OC	Schizosaccharomyces pombe (Fission yeast).	Db	64	FEEBRDFMILDRYEOKCPFPFLYTGRGGSSDSXHLGHNIPPMCKWLGQDVQFLVQT	123
CC	CC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	Oy	127	DBBKYLWKD-LTLDQAVGDAVENAKDIIAGPFDINKKFIFSDUDYMGNSGFEVKNNVVIQ	185
CC	CC	Schizosaccharomycetales; Schizosaccharomycetaceae.	Db	124	DDEKEFLPKQVSLEDCQFARAEKAYDIAVGEPEKTFPANISTYVG-GMFQNIVVIR	181
OX	NCBI_Taxid:4896;	[1]	RN			
RP	SEQUENCE FROM N.A.		Qy	186	KHYTENQVKGIFGFTDSCPGKISFPAQIAFSNSNPQIIFDRTDIOLCLPACIOPF	245
RC	STRAIN=972;		Db	182	KCTTANQSACRGTDSIGSKHFASTQASQFSSPHIFNGAKDPCL-PAIDDP	241
RX	MEDLINE=21848401; PubMed=11859360;		Oy	246	YFRMTRDVAEPRIGYPKDALHSTTEFPALOGZCFTMSASDPNSIIEFLNTTAQKTKYKHK	305
RA	Brooks X., Brown D., Brown S., Chillingworth T., Churcher C.M.,		Db	242	YFRLTDWSGRKAFKCPDALLSHRFPPALQGPQFSRMSAKSDSSAIFMTTPNKTKNTRH	301
RA	Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,		Oy	306	AESGGGRDTIEERBROFGGNCNDVSEMXLTFEELDDDKLEQIKXDYTSGAMLTOBLEKKLI	365
RA	Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,		Db	302	ATSGGGATTCEREGKPNPDPDVAYQYLISFEULDDDEKLKGQLUNTYRAGTLSGEMKGCTI	361
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,					
RA	Holroyd S., Hornsby T., Howard S., Hunt S., Jagels K.,					
RA	Jones K., James L., Jones M., Leather S., McDonald S., McLean J.,					
RA	Mooney P., Moule S., Munagala K., Murphy J., Niblett D., Odell C.,					
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,					
RA	Rutherford K., Buttner S., Saunders D., Seeger K., Sharp S.,		Qy	366	EVLOPLIAEHQRKEYTDELVKEFMT-PRKESF	398
RA	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,		Db	362	KLQQFVSDFQAARSKCDDEALDMFMDGSRKLEW	395
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,					
RA	Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,					
RA	Weijens I., Vanstreets B., Rieger M., Schaefer M., Mueller-Auer S.,					
RA	Fuchs M., Fritsch C., Holzer E., Moestl D., Hilbert H., Moestl D., Reinhardt R., Lehnrich H., Pohl T.M.,					
RA	Borzym K., Langer I., Beck A., Wedler H., Wambutt R., Purnelle B.,					
RA	Eiger P., Zimmermann W., Wedler H., Purnelle B.,					
RA	Goiffon A., Cadieu B., Dreano S., Gloux S., Lelaurie V., Mottier S.,					
RA	Galbeau F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,					
RA	Lucas M., Rochelet M., Gaillardin C., Talleda V.A., Garzon A., Thode G.,					
RA	F.A. Dominguez A., Revenuel J.J., Sanchez M., del Rey F., Benito J.,					
RA	F.A. Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,					
RA	F.A. Shapkowsky G.V., Ussery D., Barrell B.G., Nurse P.;					
RA	F.J. "The genome sequence of Schizosaccharomyces pombe.";					
RA	Nature 415:871-880 (2002).					
CC	- - CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA[Trp] = AMP + diaphospho + L-tryptophanyl-tRNA[Trp].					
CC	- - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC	EMBL; 250142; CAA90501.1; - .		DR	FUNCTION.		
CC	DR	PTB; S58157; S58157.	RX	MEDLINE=97197969; PubMed=9046085;		
CC	DR	GeneDB_Spomebe; SPAC2F7.13c; - .	RA	John T.R.; Ghosh M.; Johnson J.D.;		
CC	DR	InterPro; IPR02305; tRNA-synth_1b.	RT	"Identification and expression of the Saccharomyces cerevisiae cytoplasmic tryptophanyl-tRNA synthetase gene."		
CC	DR	InterPro; IPR01412; tRNA-synth_1.	RL	Yeast 13:37-41 (1997).		
CC	DR	InterPro; IPR02306; tRNA-synt_1b.	CC	- - CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA[Trp] = AMP + dirophosphate + L-tryptophanyl-tRNA[Trp].		
CC	DR	PRINTS; PRO1039; tRNA-SYNTHTTRP.	CC	- - SUBUNIT: Homodimer.		
CC	DR	TIGRFAMS; TIGR00233; tTDS; 1.	CC	- - SUBCELLULAR LOCATION: Cytoplasmic.		
CC	DR	PROSITE; PS00178; AA-tRNA_Ligase_I; 1.	CC	- - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.		
KW	Hypothetical protein; Aminoacyl-tRNA synthetase; Protein biosynthesis; KW Ligase; ATP-binding.		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
FT	SITE 91 "HIGH" REGION.		CC	Between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
FT	SITE 275 "KMSKS" REGION.		CC	DR	Z48:49; CAAB8:64:1; - .	
SEQUENCE	SEQUENCE 395 AA; 44910 MW; E656AE8B76C5DF9 CRC64;		DR	EMBL; Z71639; CA99:10:1; - .		
SQ	57.2% Score 1210; DB 1; Length 395;		DR	PIR; S51901; S519C1.		
Query Match	Best Local Similarity 59.6%; Pred. No. 5.7e-91; Indels 8; Gaps 4;					
Matches 235; Conservative 6%; Mismatches 91;						
Qy	11 EEDFDPPWTVOTS---SAKIGDIDKLVREGSSKIDKELINRERATGSRPHFLRRGI 66					
Db	4 EEQIQTVPWDYKGSIVDGEER3DIDYRLLVQFGTRKTCPELERKFLCKPHILLRRGA 63					

DR	GermOnline; 143519;	-	Crenarchaeon, Sulfolobus tokodaii strain7.;"
SGD; S000557; WRS1.	DR	GO:0000557; GO:000557; WRS1.	L-tryptophan-tRNA ligase activity; IDA.
DR	InterPro; IPR002305; tRNA_synt_1b.	DR	CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
DR	InterPro; IPR001412; tRNA_synt_1.	DR	SUBCELLULAR LOCATION: Cyttoplasmic.
DR	InterPro; IPR002306; tRNA_synt_1b.	DR	SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
DR	PRINTS; PRO1039; TRANSYNTIRF.	DR	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi-sib.ch/announce/ or send an email to license@ebi-sib.ch).
EMBL; AP000981; BAB65126.1; ALT_INIT.	CC	CC	CC
HAMAP; MF_00140; ; 1.	DR	CC	CC
InterPro; IPR002305; tRNA_synt_1b.	DR	CC	CC
InterPro; IPR001412; tRNA_synt_1.	DR	CC	CC
InterPro; IPR002306; tRNA_synt_1b.	DR	CC	CC
PF000579; tRNA_synt_1b; 1.	DR	CC	CC
DIGRAMS; PS000233; trps_1.	DR	CC	CC
PROSITE; PS00176; AA_tRNA_LIGASE_I; 1.	DR	CC	CC
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.	DR	CC	CC
FT SITE 111 120 "HIGH" REGION.	DR	CC	CC
SEQUENCE 295 299 "MSKS" REGION.	DR	CC	CC
SQ 432 AA; 49350 MW; C408E169737E9736 CRC64;	DR	CC	CC
Query Match 55.0%; Score 1163; DB 1; Length 432;	CC	CC	CC
Best Local Similarity 54.8%; Pred. No. 4.3e-87;	CC	CC	CC
Matches 217; Conservative 71; Mismatches 100; Indels 8; Gaps 3;	CC	CC	CC
Q1 7 ATEAAEDFDPWTY----QTSSAKGIDYDKLIVRGSSKIDKELEINRERATGQBPHHF 61	DR	CC	CC
19 STDVQEQQVTPWDVEGGVDEQRAQRTDYDKLKLQKPSGKTPVNESETLKRFQYTGEPHHPF 78	DR	CC	CC
Q3 62 LRRGGFFSHRDMMQVLDAYENKKPFLYTRGRGPSSZAMHYGLIPPTFTKMLQDVENVPL 121	DR	CC	CC
79 LRKGFLFSESERDTKFLDKLFLQGKPFELTYTRGRGPSSDSMHLGHMIPPVFKNTFQLQEVFDVPL 138	DR	CC	CC
122 VIQMTDDEXYLWK-DLTLDQAYGDAVENAKDITACSDFDINKTFIFSDLYGMMSGFYKN 180	DR	CC	CC
139 VIELDDEKEFLFKHKTINDVKNPARENAAKLLAWFDPKNTFPLSQLDQLQNG--GAFYET 196	DR	CC	CC
Q4 181 VVKLQKHVTENQVKSGIPEGFTSDCIGKISPFPAIQMPSNSFNPQIFRDRTDIQLCLIPCA 240	DR	CC	CC
197 VVRVSQITGSTAKAVFGENDSICIGKEFHAFS1QATAFPSSPNVLGPDKTCPLCLIPCA 256	DR	CC	CC
Q5 241 IDQDPYFRMTDVAPIGYPKPALLISTFFALQAGTQNSASDPNNSIFUTDTAXQIKT 300	DR	CC	CC
257 IDQDPYFRVCRDALKYSKPALKHSRFPFALQGSTTOSASDDTTAIETDTPKQIQK 316	DR	CC	CC
301 KVNHAFASGGGRDTIIEHROFGGNCDVDSPFMNLTFFLEDQDXLQTRKDYSITGAMLTGEL 360	DR	CC	CC
317 KINHKAFTSGQSVADLHRECGGNPDVVAQYLSFFKDDIVFLKCYDKYTKSGEDLSGEM 376	DR	CC	CC
361 KKALIEVLOPLIAHQARKEVTDIETVKEMTRKL 396	DR	CC	CC
377 KKLCIBTLOEFVKAFOERRAQDVDEBTLDKEMVPHXL 412	DR	CC	CC
RESULT 7	DR	CC	CC
SYN_SULTO STANDARD; PRT; 381 AA.	DR	CC	CC
Q976M1; ID_SULTO SEQUENCE FROM N.A.	DR	CC	CC
28-FEB-2003 (Rel. 41, Created)	DR	CC	CC
28-FEB-2003 (Rel. 41, Last sequence update)	DR	CC	CC
28-FEB-2003 (Rel. 41, Last annotation update)	DR	CC	CC
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophanyl-tRNA synthetase (EC 6.1.1.2))	DR	CC	CC
TRRS OR ST0159.	DR	CC	CC
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;	DR	CC	CC
Sulfolobus tokodaii.	DR	CC	CC
NCBI_TaxID:111955;	DR	CC	CC
RN	SEQUENCE FROM N.A.	CC	CC
RP MEDLINE=JCM 10545 / 7;	DR	CC	CC
RX PMID=12456156; PubMed=11572479;	DR	CC	CC
PA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi A., Hosoya S., Nagai Y., Nishizawa K., Otsuka R., Nakazawa H., Takamatsu Y., Yoshizawa T., Tanaka T., Kudoji Y., Yamazaki J., Kushida N., Onuchi A., Oishi K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.	DR	CC	CC
OC "Complete genome sequence of an aerobic thermoacidophilic	DR	CC	CC
OX RT TRPS OR SS00452.	DR	CC	CC
RESIDUE 8	SYN_SULTO	STANDARD;	PRT; 380 AA.
ID Q972X0; ID_SULTO	AC	Q972X0;	Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)	DT	28-FEB-2003 (Rel. 41, Last annotation update)	DT
DT 28-FEB-2003 (Rel. 41, Last annotation update)	DT	28-FEB-2003 (Rel. 41, Last annotation update)	DT
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophanyl-tRNA synthetase (EC 6.1.1.2))	DE	DE	DE
DB (TRPS).	DB	DB	DB
GN TRPS OR SS00452.	GN	GN	GN

OS	Sulfolobus solfataricus	SEQUENCE FROM N.A.	368 LQPLIAEHHQARRKEVTDIYKEFMTPRKLS	397
OC	Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;			
OX	Sulfolobus			
RN	KOBII_TAXID=2287;			
R2	[1]			
R3	SEQUENCE FROM N.A.			
R4	RESTRAIN-ATCC 35092 / DSM 1617 / P2; MEDLINE-2133296; PubMed=11427726;			
R5	She Q., Singh R.K., Conflanier F., Zivanovic Y., Allard G., Ayavez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Brauso G., Fletcher C., Gordon P.M.K., Heukamp de Jong T., Jeffries A.C., Kozares C.J., Medina N., Peng X., Thi-Ngoc H.P., Reeder P., Schenk M.E., Therriault C., Tolstrup N., Charlebois R.L., Doolittle W.F., Duguet Y., Gaasterland T., Garrett R.A., Ragan M.A., Sansen C.W., Van der Oost J.,			
R6	*The complete genome of the crenarchaeon <i>Sulfolobus solfataricus</i> P2.,"; Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).			
R7	-!- CATALYTIC ACTIVITY: ATP + L-tryptophanyl tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).			
C1	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
C2	-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.			
C3	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	CC			
DR	DR HAMAP; MF_00140; T_1.			
DR	DR InterPro; IPR002305; tRNA-synt_1b.			
DR	DR InterPro; IPR001412; tRNA-synt_1.			
DR	DR InterPro; IPR002306; tRP_tRNA-synt_1b.			
DR	DR PF00579; tRNA-synt_1b; 1.			
DR	DR PRINTS; PRO0039; TRNA-SYNT-TRP.			
DR	DR TIGRFAMS; TIGR00233; tRPS_1.			
DR	DR PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE NEG.			
KW	KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;			
KW	KW Complete proteome.			
FT	FT SITE 81 89 "HIGH" REGION.			
FT	FT SITE 253 257 "RSRS" REGION.			
SEQUENCE	SEQUENCE 380 AA; 44691 MW; CF8344CF639835680 CRC64;			
Query	Query Match Score 905; DB 1; Length 380;			
Db	Best Local Similarity 48-7%; Pred. No. 3-5e-66;			
Db	Matches 190; Conservative 68; Mismatches 108; Indels 24; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 825; DB 1; Length 385;			
Db	Best Local Similarity 45.9%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 39.1%; DB 1; Length 385;			
Db	Best Local Similarity 39.1%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 12.9%; DB 1; Length 385;			
Db	Best Local Similarity 12.9%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 180; Conservative 69; Mismatches 116; Indels 27; Gaps 10;			
Db	FT SITE 253 257 "HIGH" REGION.			
Db	SEQUENCE 385 AA; 45178 MW; KMRS" REGION.			
Query	Query Match Score 11.5%; DB 1; Length 385;			
Db	Best Local Similarity 11.5%; Pred. No. 8-8e-60;			
Db	Matches 1			

Q	249 MTRDVAIRGKPKPALLSTEFFPALQAGTQTKNSASDPNIS; EFTDTAKQIKTKVNKAHS	308	Oy	71 RDNGQVLDAYENKKPKPFYLYTGGRSPSSSEAMHGCHLIPETITKNTQDVENVPLQMTDDEK	130
Dt	223 LQRDFALSLGTYKTRALHSKEFPPLTGHLEGKMSASKPETA; YLTIDNSEEAGKCKIMKALT	282	Db	59 RDYDKVLDYEEBRGFFFLYTGRG2SG- PMHIGHIIIPPEFKTKWQEKERWONLYQI7DDEK	117
Q	309 GGRDTLEEHFRQGNCNDYDSMNYLTFLEDDKXLEQIRKDY--TSGSAMITGELKKALI	365	Qy	131 YLMKPC-1LTUDQAYGDAVENAKCQITACGPDINKTPFIPSDDLYMGMSGPYYKNTVKLQKEV	169
Dt	283 GGQPTLKQKREKGNGPCKVQVZKWLLEFPEPDK-K- KLMERYYACKNGELLGECKRYLI	340	Db	118 PFKKENETPDKHWAVENTLTDIAVGDPDKEKFQNSEF---TKYEMATPIAKIN	173
Q	366 EVLQPLAERQARRKEVTEYFMPRKL	397	Qy	190 FNOVKGLFGFTSDCIGKISPAIQAPSFSNSFPOQIFRDRDTQCLICPAIDQDPYRMR	249
Dt	341 QRVQEFLKHKHQEKRKK-AEKLVFKYTGKLA	371	Db	174 FSWAKAFGGTEOSKGMIEPPAQIAPT-----FEKR--RCLIPAAQDQDPWRL	223
<hr/>					
Q	SYN_S1_N_PYRAB	STANDARD;	Db	250 TRDVAAPRIGYPKPEALHSTFPALQAGTQTKNSASDPNIS; EFTDTAKQIKTKVNKAHS	309
Q	SYN_IT_PYRAB	STANDARD;	Db	224 QEDFAESLGYYKTAIIHSKFVPSLTSLGGSNSASKPTRA-YLTDSPEBVKEKVWKEALT	283
AC	Q9UY11;		Qy	310 GRTDIESHRQEGGNCDVDSMENYLTFPLEDDDKLQEQRKCY--TSGAMLTGELKKALI	356
DI	28-FEB-2003	(Rel. 41, Created)	Db	284 GRPTLKEQRBKCGEPEKCVWFKMLLEFFEDDK-K-KLKERYYACKNGELTCBCKRYLIS	341
DT	28-FEB-2003	(Rel. 41, Last sequence update)	Qy	367 VLPQLIAEHQARKEVTDIVK	388
DB	10-OCT-2003	(Rel. 42, Last annotation update)	Db	342 KIQEF-LKEHQKERKKAEKQIEK	363
DB	TRYPHOPHAN-tRNA synthetase (EC 6.1.1.2) (tryptophan--tRNA ligase)				
DB	(TRYPHOS)				
GN	TRPS OR PYRAB16970 OR PAB1111.				
OS	Pyrococcus abyssi.				
OC	Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;				
OC	Pyrococcus.				
NCBI_TaxID	=29292;				
RN					
RP	SEQUENCE FROM N.A.				
RC	SEQUENCE FROM N.A.				
RX	STRAIN=GB5 / Orsay;				
RX	MEDLINE=2511515;				
RA	Cohen G.N., Barbe V., Flament D., Galperin M., Heiling R., Leconte O.,				
RA	Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,				
RA	Van der Oost J., Wissenbach J., Zivanovic Y., Forterre P.,				
RA	An integrated analysis of the genome of the hyperthermophilic				
RT	archaeon Pyrococcus abyssi.				
RL	Mol. Microbiol. 47:1495-1512(2003).				
CC	-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +				
CC	diphosphate + L-tryptophanyl-tRNA(Trp).				
CC	-!- SUBCELLULAR LOCATION: Cytoplasmatic.				
CC	-!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.				
CC					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC					
CC	EMBL: AB248288; CAB50601.1; -				
CC	PIR: C75020; C75020.				
CC	PIR: MF_00140; -; 1.				
CC	InterPro: IPR002305; tRNA-synt_1b.				
CC	InterPro: IPR001412; tRNA-synt_1.				
CC	Complete proteome.				
CC	SITE 82 90 "HIGH" REGION				
CC	SITE 253 257 "RMGSKS" REGION.				
CC	SEQUENCE 385 AA; 451:00 MR;				
CC	4C29D01414976B12 CRC64;				
CC					
CC	Query Match 37.9% Score 803; DE 1; Length 365;				
CC	best Local Similarity 45.3%; Pred. No. 7:2e-58; Gaps 9;				
CC	matches 173; Conservative 63; Mismatchs 120; Indels 26;				
CC					
DR	EDF VDPEVTVQTSSPARGTDYDYLIVRGSSKIDLEINRIERATQRPHEHLRGIFFSH	70	DR	AP000007; BA31046.1; M17_INIT.	
DR	3 ED-FKTVPNEVEGV--VDYNKLIEHFGTSPLTEELKTAELTKSELPLFFRKFFFH	58	DR	HAKP; MF_00140; /1.	
DR			DR	IPR002305; tRNA-synt_1b.	
DR			DR	InterPro; IPR001412; tRNA-synt_1.	
DR			DR	InterPro; IPR002306; tRNA-synt_1b.	
DR			DR	Pro0579; tRNA-synt_1b.	
DR			DR	PRINTS; FR01039; TRNAINTHRE.	

E3 TIGRFAM6; TIGR0233; tRPS; 1.	CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
D2 PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.	CC
K1 Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;	CC
K1 Complete proteome.	CC
F1 SITE 82 90 "HIGH" REGION.	CC
F2 SITE 253 90 "KMSKS" REGION.	CC
S2 SEQUENCE 386 AA; 45305 MW; 9E3C392F1028B2DD CRC64;	CC
Query Match Score 796; DB 1; Length 386;	DR EMBL: AE00911; ALA6664..1; -
Best Local Similarity 44.0%; Pred. No. 2.7e-57;	DR HAMAP: MF_00140; -; 1.
Matches 172; Conservative 68; Mismatches 125; Indels 26; Gaps 9;	DR InterPro: IPR002306; TPP_tRNA_Synt_1b.
Qy 11 BBDFDPEWVTVQSSAKGIDYDRLIVRGSSKIDKELINRERATGQRPHFLRRGIFFSH 70	DR InterPro: IPR002105; TPP_tRNA_Synt_1b.
Db 3 BEPKTPWEGU --VDEDKLIRKNGTSLTDELKETABLTKSLELPFIRRKEFFSH 58	DR PRINTS: PR01039; TRNA_Synt_1b.
Qy 71 RDMDNOVLDAYENKCPDFYLTYGRGRPSSSEAMHVGHLIPFKLQLQDVENVLVICQDDEK 130	DR TIGRFAM6; TIGR00233; tRPS; 1.
Db 59 RYDILKQYBEGRGGFPLTYGRGPSC-PMHTGHIIFFATKWLQSKFQGVNLQYIQTIDDEK 117	DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Qy 131 YIMKD-LTLDQAYGDAVENAKDIIAGCFDINKTRIFSDLYMGMSQSGFYKVNVRQKFT 189	DR KMSKS; Protein biosynthesis; Ligase; ATP-binding;
Db 118 FLFKENLTPEDDTKPWAYDNLLAVGFDPPDTKFIFQNSFE---TKIYEMAIPIAKKIN 173	DR Complete proteome.
Qy 190 FNGVKGIGPTDSDLIGKSFPAQAPSNSNFPQIIFRDTDCOLICPAIDQDPYFRM 249	FT SITE 81 89 "HIGH" REGION.
Db 174 FSKMAKAVFGETEQSKIGMIFPPACIAPTE----FEK---FCLLPAIDQDPYWR 223	FT SITE 258 262 "KMSKS" REGION.
Qy 253 TRDVAAPRIGYPKPALKLHSSTFPALQGAQTPMSASDPNNSIPLTDATAKQIKTKMKHAFSG 309	SQ SEQUENCE 375 AA; 43178 MW; 3DDBF852D680F116 CRC64;
Db 224 QRDAAESLGYYKTAHLHSKVPVLSLTSGLMSASKPETYLTSPDVEKKWKFPLTG 283	Query Match Score 735; DB 1; Length 375;
Qy 310 GRDTLEEHFROFGNCNDVDSMEMLTFEYEDDDKLEQIRKDY--TSGSAMLTGEKLKALIE 366	Best Local Similarity 41.6%; Pred. No. 2.4e-52;
Db 284 GRPLKLEDEBKGGPEKECVFVKNEIIFEDDK--KLKERYYACTNGE,C;GECKRYLIS 341	Matches 162; Conservative 79; Mismatches 130; Indels 18; Gaps 11;
Qy 367 VLOPLIAHQARKEVTDLIVKBNTPKLS 397	Qy 11 EEDF-TDPWTWVOTSSAKGKQYDKLIVRFGSSKIDKELINRERATGQRPHFLRRGIFES 69
Db 342 KTEPEFLKHGRKXK-AEFLVVERKTYGCLA 371	Db 2 EBEFVUTPWEYGR ---VDEDKLJHKFQAXPLTDEVALLEYKETAGE-VEPPLRREFFYA 56
RESULT 13 SYW2_HAHL1 STANDARD; PRT; 380 AA.	Qy 70 HRDMNQVLDAYENKCPDFYLTYGRGRPSSSEAMHVGHLIPFKLQLQDVENVLVICQDDEK 129
SYW_PYRAE ID SYW_PYRAE STANDARD; PRT; 375 AA.	Db 57 HRDFDEFIMKWHGEGRPWALYTGRGSQG-PVHIGHMWPWLLKWSDFKGLEVYFQITDDE 115
AC OBZTUS; AC OBZTUS; AC OBZTUS; AC OBZTUS;	Qy 130 K-YLWKLDTJDQAYGDAVENAKDIIAGCFDINKTFLPSDLYGMGSQSGFYKVNVRQKFT 188
DT 28-FEB-2003 (Rel. 41, Created)	Db 116 KFYDDPMPKLEEAATWAEYALDVALGSPSPERLIIIDIXKI---KPLIPIAVAWAKL 172
DT 28-FEB-2003 (Rel. 41, Last sequence update)	Qy 189 TNFNOVTKGIGPFTDSOPIGKTSFPAQAPSNSNFPQIIFRDTDCOLICPAIDQDPYFR 248
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2; tryptophan--tRNA ligase)	Db 173 TWNTVTKATPQGTDSNNGIYPSQIAFLET-EELRREATPV-LIPAAIDQDPYFR 228
DE tRPS .	Qy 249 MTRDVAAPRIGYPKPALKLHSSTFPALQGAQTPMSASDPNNSIPLTDATAKQIKTKMKHAFSG 309
GN TRPS OR PAE3091.	Db 229 LARDADALGYKPESTLYSKFTIMALTG-ZEKWMSASNPDASVLTDEKTYRKV-MNAT 286
OS Pyrobaculum aerophilum.	Qy 303 GGRDTIBERQFGNCNDVDSMEMLTFEYEDDDKLEQIRKDYTSGAMLTCGLKALIETVL 368
O1 Thermoproteaceae; Thermoprotei; Thermoproteales;	Db 287 GGRPZAEQEKEYGGNPENEVCPVPHYTMFLPDDAESVETKIRDCKSGALLGECKULHEK 346
O1 NCBI_TAXID-137773; [1]	Qy 369 QPLIAEHQARKEVTDLIVKBNTPKLS 397
R1 SEQUENCE FROM N.A.	Db 347 TKFLGEHRERERARGK-1DEYERLUSVKL 374
R1 STRAIN=IM2 / ATCC 51176B / DSM 7523;	RESULT 13
R1 MEDLINE=2164397; PubMed=11792889;	SYW2_HAHL1 STANDARD; PRT; 380 AA.
R1 Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Muller J.H.;	AC OBZTUS; ID SYW_PYRAE
R1 "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum,"	DT 28-FEB-2003 (Rel. 41, Last sequence update)
R1 Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).	DT 15-MAR-2004 (Rel. 43, Last annotation update)
C1 - CATALYTIC ACTIVITY: Amp + L-tryptophan + tRNA(tRPs) = AMP + diphosphate + L-tryptophanyl-tRNA(tRPs).	DE Tryptophanyl-tRNA synthetase 2 (EC 6.1.1.-2) (Tryptophan--tRNA ligase 2) (TRPS 2).
C1 - SUBCELLULAR LOCATION: Cytoplasmic.	GN TRPS2 OR TRPS OR VNG2332G.
C1 - SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.	CS Halobacterium sp. (strain NRC-1 / ATCC 700922 / SCM 110B1).
C1 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	CC Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
C1	CC Halobacteriaceae; Halobacterium.
C1 Leithauser S., Keller K., Cruz R., Danson M.J., Hough D.W.,	CX TAXID=64091;
C1	RN 11;
C1	RP SEQUENCE FROM N.A.
C1	RX MEDLINE=2050483; PubMed=1116930;
C1	RA NG W.-V., Kennedy S.P., Manairas G.G., Bergquist B., Pan M., Shukla H.D., Jasky S.R., Baliga N.S., Thorsson V., Sbragna U., Swartzell S., Near D., Hall J., Dah T.A., Welli R., Gao Y.A., Leithauser S., Keller K., Cruz R., Danson M.J., Hough D.W.,

Query Match	Best Local Similarity	Pred. No.	Matches	Indels	Gaps	17;
1.0 AEEDFVDPNTVQTTSSAKGIDYDKLIVTRGGSSKIDKEELINRLERATQRPHFLRRGIFFS 69	35.4%	76	Mismatches	-40;		
3 ADGVNDTVPAVESDD--LYDEKULAREGDELDTQARAFP----DHLPLNRLFYA 53						
7.0 HRDMNQVLDAYENKKPFYLYTGRGPSEAMXVGHLIPEFIKWLQDVENKPELVIGMTDDE 129						
54 GRDVFDFLTAGEQS---IVTGIVGPGS-PMHGLHAMMVFYFARRLQQZFGARVYVPSDDE 108						
1.30 KYLWKDILTDQAYDAVE-NAKDLIAQGEDINKTFLF---SDJDM-GMSGGEXXWVKI 184						
109 KYWFKDQCPAET-CDYLRNLRLDVAQGDPELTRIVVDTRADVYPLATAFAGD--- 164						
1.85 QKHVTENQVKGKGFDSDCIGKISPAQIAQAPSNSNPQIFRDRDTIQCLIPAIQDQ 244						
J65 -RHATLQNVYG---EPDNGVOAFPVQVTAHLL--IPOLVNG- EHTLVLVIAVDQD 213						
245 PYFRMRDVAPIRGYP--KPALLESTFPPEALOGAQTMKSASDPNNSFQIFRDRDTIQCLIPAIQDQ 302						
214 PHVRVSRDVAAKARYPVKGPKGALLMQFLPSLAG- PGKMSSS-AGYSLRLTDSPDTREKV 271						
303 NGHAFTSGSRDTIBERHQFGNCNDVFSMMLTFPLEDDD-KLEQTRKDTSGAMITGEK 361						
272 RTHAYTGRGRASVSEHRAGGVPAEDVPPOTYLSAFFFDDAELARIEYERAGDLISGELK 331						
362 KALIEVQQLIAHQARKEVTDIYKEPMTPKLSD 399						
332 DIAADRTEFIAHQRAALGD-VTEALDAFPLDD 367						

				PW--ETPAV--IDYKCKTMEQFGVKP:VIVDVLGDLIKEE-----HFFERNILGERDFERI	57
Db	273	AKCGGATLBEHRGGNPDECYELMYHLADIGGDEKLRETRIKCREGGDIICECK	332		
Qy	362	KALIEVQLBLIAHQARRKEVTDI	386		
Db	333	RNGGEALABILELEERRRDVDEL	357		
	RESULT 15				
	SYN_MEJJA	STANDARD;	PRR;	370 AA.	
AC	058810;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)				
DB	(TPRS)				
GN	TRPS_CRMJ415.				
OS	Methanococcus jannaschii.				
OC	Euryarchaeota; Methanococcales;				
OC	Methanococcales; Methanococcaceae; Methanococcaceae.				
OX	NCBI_TAXID=190;				
RN	SEQUENCE FROM N.A.				
RC	STRAIN-JAL-1 / DSM 2661 / ATCC 44067;				
RX	MEDLINE=9637999; Pubmed=8658087;				
RA	Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage R., Dougherty B., Tomb J.F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.P., Weinstock K.G., Merrick J.M., Glodck A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovskiy M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii," Science 273(5):1058-1073(1996).				
C1	-1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophyl-tRNA(Trp).				
C2	- SUBCELLULAR LOCATION: Cytoplasmic.				
C3	-1- SIMILARITY: Belongs to class I aminoacyl-tRNA synthetase family.				
C4	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license/agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
D1	EMBL; U67582; AAB99425.1; -.				
D2	PIR; F64476; F64476.				
D3	TIGR; MJ1415; -.				
DR	HRMAP; MF_00140; -.				
DR	InterPro; IPR002305; tRNA-synt_1b.				
DR	InterPro; IPR001412; tRNA-synt_1.				
DR	InterPro; IPR002306; Trp_tRNA_synt_1b.				
DR	PFAM; PF00519; tRNA_synt_1b; 1.				
DR	PRINTS; TIGR0033; TIPS; 1.				
DR	PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.				
KW	Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.				
FT	SITE 75 83 "HIGH" REGION.				
FT	SITE 255 259 "RNSKS" REGION.				
SEQUENCE	370 AA; 24660 MW; B6C71.07CFB2B59D CRC64;				
Query Match	19.4%	Score 409.5;	DB 1;	Length 370;	
Best Local Similarity	30.9%;	Pred. No. 7e-26;			
Matches	119;	Conservative 72;	Mismatches 153;	Indels 41;	Gaps 16;
Qy	FWTQQTSAKGIDYDKULVRFGGSKIDELINIERATGQRPHFLRLGIFFHRDNQV 76				

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

August 24, 2004, 17:42:41 ; Search time 117 Seconds

(without alignments;
1081.391 Million cell updates/sec
1 SNHGDATAEEDFVDPPTV.....VTDBIVKEEFTPKLISFDQQ 401

Perfect score: 2116

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL:25:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_organelle:*

8: sp_phage:*

9: sp_plant:*

10: sp_rdent:*

11: sp_virus:*

12: sp_vertebrate:*

13: sp_unclassified:*

14: sp_rvirus:*

15: sp_bacteriap:*

16: sp_archeap:*

17: sp_archaea:*

17: 31.0 14.7 11.1 5 Q95Y18 encephalito
18: 296.5 14.0 13.6 6 Q9TS88
19: 294 13.9 15.7 5 Q9U533
20: 286 13.5 10.9 4 Q9UD15
21: 269.5 12.7 51.3 1 Q9HR83
22: 203.5 9.6 341 16 Q8EJ5
23: 203.5 9.6 341 16 Q8DWP7
24: 191 9.0 324 17 QBTXZ2
25: 189 8.9 364 17 Q9YA64
26: 185.5 8.8 366 16 Q8AIC7
27: 181.5 8.6 331 17 Q9T521
28: 181 8.6 340 16 Q8DS81
29: 178 9.4 340 16 Q87Q93
30: 174 8.2 334 16 Q83J38
31: 171.5 8.1 351 10 P93018
32: 171.5 8.1 356 16 Q83A61
33: 170.5 8.1 376 5 Q7YYAQ
34: 167 7.9 351 16 Q9RVD6
35: 166.5 7.9 338 16 Q882B4
36: 164.5 7.8 377 5 Q86A90
37: 164.5 7.8 895 16 Q9SGN2
38: 158.5 7.5 375 16 Q8AAG1
39: 158.5 7.5 375 17 Q9WQ27
40: 156 7.4 372 17 Q823TT
41: 154.5 7.3 302 1 Q07119
42: 153.5 7.3 317 17 Q8PSI:
43: 152.5 7.2 682 5 Q9N988
44: 152 7.2 317 17 Q8PJK0
45: 149.5 7.1 327 17 Q9EN62
Q9hn62 halobacteri

ALIGNMENTS

RESULT 1

Q9DC65 PRELIMINARY; PRT; 475 AA.
ID Q9DC65:
AC Q9DC65:
DT 01-JUN-2001 (TRMBLrel. 17, Created)
DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Adult male lung cDNA, RIKEN full-length enriched library
DE clone:1200002C07, full insert sequence.
GN WARS.
OS Mus musculus (Mouse).
OC Bokaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthezia; Rodentia; Sciurognathi; Muridae; Murinae; Mcs.
RN [1]
RN SEQUENCE FROM N_A.
RN SEQUENCE FROM C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyoawa H., Kondo S., Yamamoto I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Matsukawa H.A., Ashburner M., Batalov S., Gaasterland T., Gissis C., King B., Kochiwa H.,
RA Fleischmann W., Kuehl P., Lewis S., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
RA Gustincich S., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarello L., Montaerts P.,
RA Nordone P., Ring B., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690 (2001).
DR EMBL; AK004541; BAB233571; -.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1957	92.5	475	11	Q9DC65	Q9dc65 mus musculus
2	1957	92.5	481	11	Q9U584	Q9u584 mus musculus
3	1953	92.3	475	11	Q8OZY4	Q8ozy4 mus musculus
4	1820	86.0	475	13	Q7ZWT7	Q7zwt7 xenopus lae
5	1537	72.6	305	11	Q70184	Q70184 cavia porce
6	1374.5	65.0	420	5	Q9U4Y0	Q9u4y0 drosophila
7	1374.5	65.0	430	5	Q9U4Y1	Q9u4y1 drosophila
8	1370	64.8	430	5	Q9VHG2	Q9vhg2 drosophila
9	1323	62.5	417	5	Q9U1R2	Q9u1r2 caenorhabdit
10	1301	61.5	402	10	Q9SR15	Q9sr15 arabidopsis
11	1209	57.1	491	5	Q870u0	Q870u0 neurospora
12	1026	48.5	632	5	Q8IDW3	Q8idw3 plasmodium
13	942	44.5	385	5	Q8SQY5	Q8sqy5 encephalito
14	795.5	37.6	490	5	Q9U1FS	Q9u1fs leishmania
15	682	32.2	136	6	Q95295	Q95295 sus scrofa
16	400.5	18.9	165	10	Q7XY51	Q7xy51 griffithsia

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

DR	MGI:104630; Wars.	DR	InterPro; IPR001412; tRNA-synt_I.
DR	GO:0005524; F:ATP binding; IEA.	DR	InterPro; IPR002306; tRNA-synt_1b.
DR	GO; GO:0006336; P:tryptophanyl-tRNA ligase activity; IEA.	DR	InterPro; IPR000738; WHEP-TRS.
DR	GO; GO:0006336; P:tryptophanyl-tRNA aminoacylation; IEA.	PFam; PF00579; tRNA-synt_1b; 1.	
DR	InterPro; IPR002305; tRNA-synt_1b.	DR	PFam; PF00458; WHEP-TRS; 1.
DR	InterPro; IPR001412; tRNA-synt_I.	PRINTS; PRO1039; TRYPTOPHANYL-TRNA synthetase.	
DR	InterPro; IPR002306; tRNA-synt_1b.	DR	TIGRFAMS; TIGR00233; tRPS; 1.
DR	InterPro; IPR000738; tRNA-synt_1b.	DR	PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
PFam; PF00579; tRNA-synt_1b; 1.	DR	PROSITE; PS00762; WHEP TRS; 1.	
PFam; PF00578; WHSP-TRS; 1.	DR	Aminoacyl-tRNA synthetase.	
PRINTS; TIGRFAMS; TIGR00233; tRPS; 1.	SEQUENCE	481 AA;	54325 MW; A754E1DDF50E2EF3 CRC64;
SEQUENCE 475 AA; 53641 MW; C346TPE85521DE4C CRC64;	SC	Query Match 92.5%; Score 1957; DB 11; Length 481;	Score 1957; DB 11; Length 481;
Best Local Similarity 91.5%; Pred. No. 6.7e-163;	SC	Best Local Similarity 91.5%; Pred. No. 6.8e-162;	Pred. No. 6.8e-162;
Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;	SC	Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;	Matches 366; Conservative 20; Mismatches 14; Indels 0; Gaps 0;
Qy 2 NHGPDAAEEDVDPDTQVTSKAKGIDKDKLIVRPPSSKKDKEELNIRERATGQRPHF 61			
Dt 76 NCDSDATKASEDFVDPTVTRTSSAKGIDKDKLIVQFQSSSKDKEELNIRERATGQRPHF 135			
Qy 62 LRRGIFSHRDNNQVLDAYENKPKFLYTGROSSSEAMHVGHLLPFITKWLQDVNVPL 121			
Dt 136 LRRGIFSHRDNNQVLDAYENKPKFLYTGROSSSEAMHVGHLLPFITKWLQDVNVPL 195			
Qy 122 VIQMTDDEKYLWMDLTLDQDAYDVAENAKDILACGEFDINKTEFSQDLYMGMSGFVKVN 181			
Dt 196 VIQMSDDEKYLWMDLTLDQDAYDVAENAKDILACGEFDINKTEFSQDLYMGMSGFVKVN 255			
Qy 182 VKIQKHYTENQVKGIFGTDSQIGKISRPVQADPSNSPQFQFDRDQLQCLPCAI 241			
Db 256 VKIQKHYTENQVKGIFGTDSQIGKISRPVQADPSNSPQFQFDRDQLQCLPCAI 315			
Qy 242 DQDPYFMRMTDVAAPRIGPKALHLSPFPALQGAQIKMSADPNSSIFLTDTAQJQTK 301			
Db 316 DQDPYFMRMTDVAAPRIGPKALHLSPFPALQGAQIKMSADPNSSIFLTDTAQJQTK 375			
Qy 302 VNKAHFSGGRDTIEHQFGNCDVDSFMYLTFFLEDDKLEQIKRDYTSGAMLTGELK 361			
Db 376 VNKAHSGGGRDTVEERQEGGNCEVDVSFMYLTFFLEDDKLEQIKRDYTSGAMLTGELK 435			
Qy 362 KALIEVLOPLIAHQARRKEYTDEIVKEFMPTRKLSEDFQ 401			
Db 436 KTLIDVLOPLIAHQARRKEYTDEIVKEFMPTRKLSEDFQ 475			
RESULT 3 QBOZY4 PRELIMINARY; PRT; 475 AA.			
ID 099J58 PRELIMINARY; PRT; 481 AA.			
AC 01-JUN-2001 (TREMBLref: 17, Created)	AC 01-JUN-2001 (TREMBLref: 17, Last sequence update)	AC 01-JUN-2001 (TREMBLref: 17, Last sequence update)	AC 01-JUN-2001 (TREMBLref: 17, Last sequence update)
DT 01-JUN-2001 (TREMBLref: 17, Last sequence update)			
DT 01-OCT-2003 (TREMBLref: 25, Last annotation update)			
DB Tryptophanyl-tRNA synthetase.	DB Tryptophanyl-tRNA synthetase.	DB Tryptophanyl-tRNA synthetase.	DB Tryptophanyl-tRNA synthetase.
GN Wars.	GN Wars.	GN Wars.	GN Wars.
Mus musculus (Mouse).	Mus musculus (Mouse).	Mus musculus (Mouse).	Mus musculus (Mouse).
OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	NCBI_TaxID=10090;	NCBI_TaxID=10090;	NCBI_TaxID=10090;
RN 1.1	RN 1.1	RN 1.1	RN 1.1
RP SEQUENCE FROM N.A.			
RC TISSUE-Breast tumor;	RC TISSUE-Breast tumor;	RC TISSUE-Breast tumor;	RC TISSUE-Breast tumor;
RA Strausberg R.;	RA Strausberg R.;	RA Strausberg R.;	RA Strausberg R.
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.			
EMBL; BC003450; AAH03450; -.			
DR GO: GO:0005524; F:ATP binding; IEA.			
DR GO; GO:0006436; P:tryptophanyl-tRNA ligase activity; IEA.			
DR GO; GO:0006436; P:tryptophanyl-tRNA aminoacylation; IEA.			
DR InterPro; IPR002305; tRNA-synt_I.			
DR PRINTS; PRO1039; TRYPTOPHANYL-TRNA synthetase.			

L3	TIGRFAMS; TIGR00233; ttrs; 1.	Query Match	86.0%	Score 1820;	DB 13;	Length 475;
L3	PROSITE; PS00178; AA; tRNA_LIGASE_I; 1.	Best Local Similarity	83.2%	Pred. No. 6.3e-151;		
L3	PROSITE; PS00178; WHBP-TRS; 1.	Mismatches	39;	Mismatches	28;	Indels 0;
EV	Aminoacyl-tRNA synthetase.	Matches	333;	Conservative		Gaps 0;
S2	SEQUENCE 475 AA; 53613 MW;					
Query Match						
Best Local Similarity 91.2%; Pred. No. 1.5e-162;						
Matches 365; Conservative 20; Mismatches 15; Indels 0; Gaps 0;						
CY	2 NHGDPATRAEEDFVDPWTVOTSAKGIDYDKLIVRGSSKIDKEKLINRERATGORPHF 61	Qy	1 SNHGDPATEASEDFVDPWTVOTSAKGIDYDKLIVRGSSKIDKEKLINRERATGORPHF 60			
I5	76 NCDSATAKEDFVDPWTAITSAKGIDYDKLIVRGSSKIDKEKLINRERATGORPHF 135	Db	76 NRNGPSTNDGDDFVDPWTVOTSAKGIDYDKLIVRGSSKIDKEKLINRERATGORPHF 60			
I5	62 LRGIFPSHDMQVQLDAVENKPKLYTGRGPSSAMHGHLPPEFTKWLQDVENVVP 121	Qy	61 FLRRGIFFFSHDMQVQLDAVENKPKLYTGRGPSSAMHGHLPPEFTKWLQDVENVVP 120			
Db	136 LRGIFFFSHDMQVQLDAVENKPKLYTGRGPSSAMHGHLPPEFTKWLQDVENVVP 195	Db	136 FLRRGIFFFSHDMQVQLDAVENKPKLYTGRGPSSAMHGHLPPEFTKWLQDVENVVP 195			
CY	122 VIONTDDKEYLWKLDTLDQAYDAVENAKDIIACGFDINTKFISFDDYMGMSGFYKRY 181	Qy	121 LYIOMTDDKEYLWKLDTLDQYGDAVENAKDIIACGFDINTKFISFDDYMGMSGFYKRN 180			
Db	196 VIONSDDEKEYLWKLDTLDQYNSYTENAKDIIACGFDINTKFISFDDYMGMSGFYKRN 255	Qy	121 LYIOMTDDKEYLWKLDTLDQYGDAVENAKDIIACGFDINTKFISFDDYMGMSGFYKRN 180			
CY	182 VKIQRKHVTENOKVGLFGFTSDCIGKISFPAQAAFSNSPNSFSPOLFRDTDIQCIPCAI 242	Db	196 LYVQLIDDEKEYLWKLDTLEKAYQATENAKDIIACGFDINTKFISFDDYMGMSGFYKRN 255			
Db	256 VKIQRKHVTENOKVGLFGFTSDCIGKISFPAQAAFSNSPNSFSPOLFRDTDIQCIPCAI 315	Qy	181 VVKIKQHVTENQVKGIFGFTSDCIGKISFPAQAAFSNSPNSFSPOLFRDTDIQCIPCA 240			
CY	242 DQDPYFRMTDVAPIGYPKPLAUSTFALLOGQTNSASDNPSSNISIIFTDQKIKK 302	Db	256 VVKIKQHVTENQVKGIFGFTSDCIGKISFPAQAAFSNSPNSFSPOLFRDTDIQCIPCA 315			
Db	316 DQDPYFRMTDVAPIGYPKPLAUSTFALLOGQTNSASDNPSSNISIIFTDQKIKK 375	Qy	301 KVNKAIFSGGRDTIEBHQFQSGNCDVDSFMVYTLFLEDDERLEQTKDYSSGALLTGDL 435			
CY	302 VNKHAIFSGGRDTIEBHQFQSGNCDVDSFMVYTLFLEDDERLEQTKDYSSGALLTGDL 400	Db	316 KLNKHAIFSGGRDTIEBHQFQSGNCDVDSFMVYTLFLEDDERLEQTKDYSSGALLTGDL 435			
Db	376 VNKHAIFSGGRDTIEBHQFQSGNCDVDSFMVYTLFLEDDERLEQTKDYSSGALLTGDL 475	Qy	361 KKALIEVLTQELTAHARKEVTDIETKEFMTPKLUSPDE 400			
CY	362 KKALIEVLTQELTAHARKEVTDIETKEFMTPKLUSPDE 475	Db	436 KKLTETLQPMISANCERRHITETYKQNMPPRLAEDF 475			
RESULT 5						
07C184	PRELIMINARY;	ERT:	305 AA.			
ID	070184	AC	070184	Created		
AC	070184	DT	01-AUG-1998 ([TREMBLrel]. 07,			
		DT	Created)			
		DT	01-AUG-1998 ([TREMBLrel]. 07,			
		DT	Last sequence update!			
		DB	01-OCT-2003 ([TREMBLrel]. 25,			
		DB	Last annotation update!			
		CS	Tryptophan-tRNA synthetase (fragment).			
		CS	Cavia porcellus (Guinea Pig).			
		CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		CC	OCMammalia; Buthidae; Rodentia; Hystriognathi; Caviae; Cavia.			
		RN	[1]			
		RN	Reaction: [1]			
		RC	SEQUENCE FROM N.A.			
		RC	STRAIN=Hartley; TISSUE=Spleen;			
		RC	Yang D.; Goto R.; Watanabe K.; Kobayashi Y.;			
		RC	"Identification and Cloning of Genes Whose Expressions are Elevated			
		RT	during DNFB-induced Guinea Pig Skin Delayed-type Hypersensitivity			
		RT	Reaction: [1]			
		RL	RT Subreaction: [1]			
		DR	EMBL: AB012222; BAAS288.1;			
		DR	-			
		DR	GO: GO:0005524; F: ATP binding; IEA.			
		DR	GO; GO:0004830; F: cryptophan-LRNA ligase activity; IEA.			
		DR	GO; GO:0004436; P: tryptophanyl-tRNA aminoacylation; IEA.			
		DR	InterPro; IPR002305; tRNA-synt_1b.			
		DR	InterPro; IPR002306; tRNA-synt_1b.			
		DR	Pfam; PF00579; tRNA-synt_1b.			
		DR	PRINTS; PRO1039; tRNA-SYNTHTRP.			
		KW	Aminocycl-tRNA synthetase.			
		FT	NON TER 1			
		SQ	SEQUENCE 305 AA; 34938 MW; 0937164333780EB7 CRC64;			
Query Match						
Best Local Similarity 94.4%; Pred. No. 2.4e-126;						
Matches 286; Conservative 11; Mismatches 6; Indels 0; Gaps 0;						
Qy	97 EAMHVGHLLIPFIFTKWLQDVENVPIQMTDECYKWLTLDCAYGDAVENAKOJIAAG 156					
Db	1 EAMHVGHLLIPFIFTKWLQDVENVPIQMTDECYKWLTLDCAYGDTENAKOJIAAG 60					

Q:	157 FDINKTIFIFSDIYMGNSSGFYKNTVYKIQHVTENOVKGIPGFTSDCIGKISFPPIQAA	216	Db	148 DDEKLWKLKDLYKVEDAIKLKGRENAKD1VAIGFDVNKTIFLFRNNEFVGKCPAMYQNTIRIQK	207
D:	61 FDINKTIFIFSDIYMGNSSGFYKNTVYKIQHVTENOVKGIPGFTSDCIGKISFPPIQAA	120	Qy	187 HTTENQYKGIQFTDSNCIGKISFPPIQAA;SFNSNSPPQIQRDRDTIQCLPCAIODDPY	246
Q:	217 PSFSNSFPQIQRDRDTIQCLPCAIODDPYFRTMDVAPRIGYPKPALLSTFFPALOGA	276	Db	208 CTVENQYKGIQFGFQGDSPIIGKIGPAAQAAAATSSTFPFIGSNR-KWHLCLPCAIODDPY	266
D:	121 PSFSNSFPQIQRDRDTIQCLPCAIODDPYFRTMDVAPRIGYPKPALLSTFFPALOGA	180	Qy	247 FRMTRDIVAPRIGYPKPALLSTFFPALOGACTMSASDPNNSFLITDARQIKCYNKHA	306
Qy	277 QTRKASDPNSSIELFTDQKIKTRKNGHAFSG3DITBHRQFGNCNDVDSFMYLTFP	336	Db	267 FRMTRDIVAPRIGYPKPALLSTFFPALOGACTMSASDQSAVILDTPKIKNKHA	326
Db	181 QTRKASDPNSSIELFTDQKIKTRKNGHAFSG3DITBHRQFGNCNDVDSFMYLTFP	240	Qy	307 FSGGRDTIBERHQFGNCNDVDSFMYLTFLEDDDKLQEIRKDTSGAM-TGELKKALIE	366
Qy	337 LEDDDKLEQTRDTSQGMLTGELKKALIEVQELIAHQKARRKEVTDLYKEEMTPKL	396	Db	327 FSGGRVTEBERRKLGSEVEFDSVYQKLFFLEDDAXLLEVRYAVSKGEMLTGEIKLVAE	386
Db	241 LEDDRRLQFIRKDTSQGMLTGELKKALIEVQELIAHQKARRKEVTDLYKEEMTPKL	300	Qy	367 VLOPLJAHQARKEVTDLYKEEMTPKLUSF	398
Qy	397 SFDFQ 401	301	Db	387 TLTPIVEQHQAAKU1'DEVLDKTYFELRPLKF	418
Db	SFFHQ 305				
RESULT 7					
	Q9U4Y1	6	Q9U4Y1	PRELIMINARY;	PRT;
	ID	Q9U4Y0	AC	Q9U4Y1;	430 AA.
	AC	Q9U4Y0;	DT	01-MAY-2000 (TREMBrel. 13, Created)	
	DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)	DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)	
	DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)	DT	01-OCT-2003 (TREMBrel. 25, Last annotation update)	
	DE	Tryptophanyl-tRNA synthetase (fragment).	DE	Tryptophanyl-tRNA synthetase (AT21437b).	
	GN	ATTS-TRP OR CG9735	GN	ATTS-TRP OR CG9735	
	OS	Drosophila melanogaster (Fruit fly).	OS	Drosophila melanogaster (Fruit fly).	
	OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	OC	Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;	
	OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	OC	Neoptera; Drosophilidae; Drosophila.	
	OX	Embryophyta; Drosophiliidae; Drosophila.	OX	Embryophyta; Drosophiliidae; Drosophila.	
	RN	[1]-TAXID=7227;	RN	[1]	
	RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.	
	RX	MEDLINE=99250164; PubMed=10233165;	RX	MEDLINE=99250164; PubMed=10233165;	
	RT	"WRS-85D: A tryptophanyl-tRNA synthetase expressed to high levels in the developing Drosophila salivary gland."	RT	"WRS-85D: A tryptophanyl-tRNA synthetase expressed to high levels in the developing Drosophila salivary gland."	
	RL	Scaphleron M., Brokstein P., Hong L., Aghayani A., Carlson J., Frise E., Champé M., Chavez C., Dorsett V., Dresnex D., Farfan D., Frise E., George R., Gonzalez M., Guarinilleri B., Li P., Liac G., Miranda A., Muncali C.J., Munro J., Paregas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.	RL	Scaphleron M., Brokstein P., Hong L., Aghayani A., Carlson J., Frise E., Champé M., Chavez C., Dorsett V., Dresnex D., Farfan D., Frise E., George R., Gonzalez M., Guarinilleri B., Li P., Liac G., Miranda A., Muncali C.J., Munro J., Paregas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.	
	RN	Submitted (GAN-2002) to the EMBL/GenBank/DBJ databases.	RN	Submitted (GAN-2002) to the EMBL/GenBank/DBJ databases.	
	DR	EMBL: AF125156; AAP201661; -	DR	EMBL: AF125156; AAP201661; -	
	DR	EMBL: AF07549; AA68116; -	DR	EMBL: AF07549; AA68116; -	
	DR	FlyBase; FBgn0010803; Aats-trp.	DR	FlyBase; FBgn0010803; Aats-trp.	
	DR	GO: GO:0004830; F: ATP binding; IEA.	DR	GO: GO:000524; F: ATP binding; IEA.	
	DR	GO: GO:0006436; P: tryptophanyl-tRNA ligase activity; IEA.	DR	GO: GO:0004830; F: tryptophanyl-tRNA ligase activity; IEA.	
	DR	InterPro: IPRC012305; tRNA-synt_I.	DR	GO: GO:0006436; P: tryptophanyl-tRNA aminoacylation; IEA.	
	DF	InterPro: IPRC01412; tRNA-synt_I.	DF	InterPro: IPR002305; tRNA-synt_I.	
	DF	InterPro: IPRC02306; tRNA-synt_I.	DF	InterPro: IPR002305; tRNA-synt_I.	
	PF	PF00524; tRNA-synt_1b; -.	PF	PF00524; tRNA-synt_1b; -.	
	DF	PRINTS: PRO1039; TRNA-synt_I.	DF	PRINTS; PRO1039; TRNA-synt_I.	
	DF	TIGRFAMS; TIGR00233; tRNA-synt_I.	DF	TIGRFAMS; TIGR00233; tRNA-synt_I.	
	DF	PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.	DF	PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.	
	KV	Aminoacyl-tRNA synthetase.	KV	Aminoacyl-tRNA synthetase.	
	FT	NON_TER	FT	NON_TER	
	SEQUENCE	420 AA; 46975 MW; 4AF066A2426ABB6 CRC64;	SEQUENCE	420 AA; 47985 MW; 2EF39E9BC1E9979A CRC64;	
	Query Match	65.0%; Score 1374.5; DB 5; Length 420;	Query Match	65.0%; Score 1374.5; DB 5; Length 430;	
	Best Local Similarity	64.8%; Pred. No. 6.8e-112;	Best Local Similarity	64.8%; Pred. No. 7e-112;	
	Matches	254; Conservative 61; Mismatches 76; Indels 1; Gaps 1;	Matches	254; Conservative 61; Mismatches 76; Indels 1; Gaps 1;	
Q:	7 ATEEADDFDWTQFSSARGIDYDQLIVRGSSKIDKEJINERATGQPHHEFRRGI	66	Q:	7 ATEEADDFDWTQFSSARGIDYDQLIVRGSSKIDKEJINERATGQPHHEFRRGI	66
D:	28 ATAPEDVDPWNASSNDAEVDLKLIREKGSKIDEEJARFERXIT3PAHSPTRGM	87	D:	28 ATAPEDVDPWNASSNDAEVDLKLIREKGSKIDEEJARFERXIT3PAHSPTRGM	87
Qy	67 FFSRHMNOVILDAYENKMPPELYTGRGPSSSEAMKHYLIPITKRLQDVENPLVYQMT	126	Qy	7 ATEEADDFDWTQFSSARGIDYDQLIVRGSSKIDKEJINERATGQPHHEFRRGI	66
D:	88 FFSRHDLHTLTLREQKPFYLYTRGPSSSLVGHFLVFMTRKQEFDVPLVIQLT	147	D:	38 ATAPEDVDPWNASSNDAEVDLKLIREKGSKIDEEJARFERXIT3PAHSPTRGM	97
Qy	127 DDEKYIWKDLTLDQAYDAVENAKD1IAAGDINTPFISSDLYNGMSSGFYKNUVKIOK	186	Qy	127 DDEKYIWKDLTLDQAYDAVENAKD1IAAGDINTPFISSDLYNGMSSGFYKNUVKIOK	186

RESULT 8	
Q9VHG2	PRELIMINARY; PRT; 430 AA.
Q9VHG2;	PRT; 430 AA.
01-MAY-2000 (TREMBLrel: 13; Created)	
01-MAY-2000 (TREMBLrel: 13; Last sequence update)	
01-OCT-2003 (TREMBLrel: 25; Last annotation update)	
CG9735-Pa.	
AARS-TRE OR CS9735.	"Drosophila melanogaster (Fruit fly)."
Euarteria; Archopoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; NCBI_TaxID=7227; NCBI_TaxID=7227;	Drosophila melanogaster (Fruit fly); Drosophilidae; Drosophila.
SEQUENCE FROM N.A.	
Medline:20190006; PubMed=10731132;	
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazier R.G., Champ M., Peiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman J., Botchan M.R., Bhardwari D., Brokstein P., Brotman P., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodck A., Gong F., Gorrell J.H., Gu Z., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibebewam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E./Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mathee B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nixon S., Pollard J., Puris V., Reese X.G., Palazzolo M., Pittman G.S., Pan S., Saunders R.D., Scheeler F., Shen H., Shiu B.C., Siden-Kiamos I., Simpson M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
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RA 67 FFRHMNQVLDAYENKCPFLYTGGRPSSEANHVGHLJ2FTTKWLODVENVPLVIQMT 126	Wasserman D.A., Weinstock G.M., Weissbach C., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of <i>Drosophila melanogaster</i> ," Science 287:2185-2195 (2000).
Db 98 PFSRDLHTLTURQKPKPFLYTGGRPSSEAMHVGHLJ2FTTKWLODVENVPLVIQMT 157	RN [2]
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Db 158 DDEKYLWKLDTLQAYEAKLKGRENKDIATAIGFDNKTPFLPNNULEFGCPCPAMYCNLTKQ 217	RA
Qy 187 FTYENQKIGIFGTDSIGKSFQIPEFRDQFLCLTPERIOPDY 246	RA
Db 218 CTFVNQYKGIFGSDTIGKIGEPAQAAPASSTPEIFNR-KYHCLIPADQDPY 276	RA
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Db 277 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 336	RA
Qy 307 FSGGRDTEEHQFGNCVDYPSMFLTEFLDEEKLBEQIRKDYTSGAMILCEKKALIE 366	RA
Db 337 PSGGRVTEEEHKLGQPEVDVSYQLKFELDDAKLBEVRAYSKEMLTCEKXLAVE 396	RA
Qy 367 VLQPLIAEHQARPKETDVEIKEMPFKLSF 398.	RA
Db 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
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RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
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RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
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RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
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RA 218 CVTFVNQYKGIFGSDTIGKIGEPAQAAPASSTPEIFNR-KYHCLIPADQDPY 276	RA
RA 247 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 306	RA
RA 277 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 336	RA
RA 307 FSGGRDTEEHQFGNCVDYPSMFLTEFLDEEKLBEQIRKDYTSGAMILCEKKALIE 366	RA
RA 337 PSGGRVTEEEHKLGQPEVDVSYQLKFELDDAKLBEVRAYSKEMLTCEKXLAVE 396	RA
RA 367 VLQPLIAEHQARPKETDVEIKEMPFKLSF 398.	RA
RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
SEQUENCE FROM N.A.	
RA 218 CVTFVNQYKGIFGSDTIGKIGEPAQAAPASSTPEIFNR-KYHCLIPADQDPY 276	RA
RA 247 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 306	RA
RA 277 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 336	RA
RA 307 FSGGRDTEEHQFGNCVDYPSMFLTEFLDEEKLBEQIRKDYTSGAMILCEKKALIE 366	RA
RA 337 PSGGRVTEEEHKLGQPEVDVSYQLKFELDDAKLBEVRAYSKEMLTCEKXLAVE 396	RA
RA 367 VLQPLIAEHQARPKETDVEIKEMPFKLSF 398.	RA
RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
SEQUENCE FROM N.A.	
RA 218 CVTFVNQYKGIFGSDTIGKIGEPAQAAPASSTPEIFNR-KYHCLIPADQDPY 276	RA
RA 247 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 306	RA
RA 277 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 336	RA
RA 307 FSGGRDTEEHQFGNCVDYPSMFLTEFLDEEKLBEQIRKDYTSGAMILCEKKALIE 366	RA
RA 337 PSGGRVTEEEHKLGQPEVDVSYQLKFELDDAKLBEVRAYSKEMLTCEKXLAVE 396	RA
RA 367 VLQPLIAEHQARPKETDVEIKEMPFKLSF 398.	RA
RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
SEQUENCE FROM N.A.	
RA 218 CVTFVNQYKGIFGSDTIGKIGEPAQAAPASSTPEIFNR-KYHCLIPADQDPY 276	RA
RA 247 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 306	RA
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RA 307 FSGGRDTEEHQFGNCVDYPSMFLTEFLDEEKLBEQIRKDYTSGAMILCEKKALIE 366	RA
RA 337 PSGGRVTEEEHKLGQPEVDVSYQLKFELDDAKLBEVRAYSKEMLTCEKXLAVE 396	RA
RA 367 VLQPLIAEHQARPKETDVEIKEMPFKLSF 398.	RA
RA 397 TLTPIVEQHQARKLTDDEVLDKYFELRPLK 428	RA
SEQUENCE FROM N.A.	
RA 218 CVTFVNQYKGIFGSDTIGKIGEPAQAAPASSTPEIFNR-KYHCLIPADQDPY 276	RA
RA 247 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 306	RA
RA 277 FRMTRDVAPIRGYKPAHLSTFEPLQGAOTKMSADPNSSTFLDTAQIKTKYKHA 336	RA
RA 307 FSGGRDTEEHQFGNCVDYPSMFLTEFLDEEKLBEQIRKDYTSGAMILCEKKALIE 366	RA
RA 337 PSGGRVTEEEHKLGQPEVDVSYQLKFELDDAKLBEVRAYSKEMLTCEKXLAVE 396	

Y	187	HVTENQVKIGFTSDCIGKISPAQAPSFSNSPQIFRRTDIOCLIPCAIDPY	246	QY	124	QMTDDEKJYKDLTIDANGGQRVENAKDIAAGGDINKTFPSDLDLMMGSSGFYRNWKV	183
Jb	218	CVTENQVKIGFTSDCIGKISPAQAPSFSNSPQIFRRTDIOCLIPCAIDPY	276	Db	143	QMTDDEKPLKDMKVDEAKKYYRENKKDIISVGFDPKTPKTFNNFEDY -XCEPFYENIVK	200
Y	247	FRMTRDVAAPRGYPKPCALLHSTFPALQAGTAKMSASDPNSSTFLYDTAKQIKTKVKA	306	QY	184	TOKHTTFNQVKGIFGFDSDCIGKISPAQAPSFSNSPQIFRRTDIOCLIPCAIDQ	243
Jb	277	FRMTRDVAAPRGYPKPCALLHSTFPALQAGTAKMSASDONSAYLTDPROQNKINKYA	336	Db	201	IWKVWNTQAAIFGETPEDCLGKARFPVAVAPCPASSFFIQGGRNDNPOLIPRIDQ	260
Y	307	FSGGTTGTTTBRQFGNCIDVSYFLFLDDKLEQITKDYTSGAMLTGEALKALIE	366	QY	244	DYFMRTRDVAAPRGYPKPCALLHSTFPALQAGTAKMSASDPNSSTFLYDTAKQIKTKV	303
Jb	337	FSGGTVSVEBKLGKGVPEVDVSYQLKKEFLIEDDAKLEEVRYAVSKGEMLTGEIRKLVAE	396	Db	261	DFFERMTDVAFLRKASZSLIPSTFLPALQAGTAKMSASSENCLFLSDPAQTKNKN	320
Y	367	VLOPLTAEHQARRKEVTDIETKEFMTPKLSE	398	QY	304	KHAFSGSGRDTTEHHQFGNCIDVSYFLFLDDKLEQIRKDYTSQAMLTGEALKKA	363
Jb	397	TLPTIVEQHQDARLITDEVDRYFEELRPLKF	428	Db	321	KYAFSGQQTVQEHRKGNGCDVDSYQFRFLDFDDEKLAETRENYTKGEMLSGLKAL	380
RESULT 9							
	901R2	O91R2;	PRELIMINARY;	PRT;	417 AA.		
	Q91R2;						
	01-MAY-2000	(TREMBLrel. 13, Created)					
	01-OCT-2003	(TREMBLrel. 25, Last sequence update)					
	01-OCT-2003	(TREMBLrel. 25, Last annotation update)					
	JB	C. elegans WS-1 protein (Corresponding sequence YB030A.1)					
	WS-1.						
	IS	Ceanorhabditis elegans					
	DC	Metazoa; Nematoidea; Rhabditida; Rhabditidae;					
	RA	Rhabditidae; Pelodoridae; Caenorhabditis;					
	XX	NCBI_TAXID=6239;					
	IN						
	IP	SEQUENCE FROM N.A.					
	IC	STRAIN-Bristol N2;					
	IX	PubMed=9059613;					
	DX	"Genome sequence of the nematode <i>C. elegans</i> : A platform for investigating biology";					
	LA	Science 282:2012-2018(1998).					
	NN	[2]					
	RP	SEQUENCE FROM N.A.					
	RA	*C. elegans tryptophanyl-tRNA synthetases"; Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.					
	PC	[4]					
	RA	SEQUENCE FROM N.A.					
	RA	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.					
	RA	[3]					
	RP	SEQUENCE FROM N.A.					
	RA	"C. elegans tryptophanyl-tRNA synthetases"; Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.					
	RA	[4]					
	RA	SEQUENCE FROM N.A.					
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DR	InterPro; IPR002305; tRNA-synt_1b.	DR	Pfam; PF00579; tRNA-synt_1b; 1.
DR	InterPro; IPR001412; tRNA-synt_1.	DR	PRINTS; PR01039; tRNA-SYNTTRP.
DR	InterPro; IPR002306; tRP_tRNA-Synt_1b.	DR	TIGRFAMS; TIGR00233; tTSP; 1.
DR	Pfam; PF00579; tRNA-synt_1b; 1.	DR	PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.
DR	PRINTS; PR01039; tRNA-SYNTTRP.	KW	Ligase.
DR	TIGRFAMS; TIGR00233; tTSP; 1.	SQ	SEQUENCE 491 AA; 55393 MW; C2833C847A66CLD9 CRC64;
DR	PROSITE; PS00178; AA_tRNA_LIGASE_I; 1.		
KW	Aminocycl-tRNA synthetase.		
SQ	SEQUENCE 402 AA; 45754 MW; B0BEA75E5D6CD15 CRC64;		
Query Match Score 61.5%; Best Local Similarity 60.3%; Matches 240; Conservative 66; Mismatches 88; Indels 4; Gaps 2; Sequence 402 AA; 45754 MW; B0BEA75E5D6CD15 CRC64;	57.1%; Score 1209; DB 3; Length 491; Best Local Similarity 58.6%; Pred. No. 2.7e-97; Matches 243; Conservation 53; Mismatches 97; Indels 22; Gaps 6;		
CY	6 DATEAEF--EDFEDPWTQTSASSAKOIJYKOKLIVRPGSSKIDKEELNTRIBATQPHPHFEI 63	QY	5 PDATE--AEEDFYDPWTQ--- TSASAGIDYDKLIVPFGSSCKDELNTRIBATGQ 56
I_D	7 DEREAEESSEQQVNEWEVSAAKGGRIDYKLUIDKEGCORIDESLDRYQBLTSQPEFVER 66	DB	16 FDRAKHAAKOTQDPTYNGEVDGDNVKAIDYNKLIEFGTKIDQALDPLRPTVTK 75
CY	64 RGIFSHFRDMQNLQDAYENKKPFYLTERGPSSAMHYGHLLIPPIFTKWLQDVENPVPLI 123	QY	57 RPHFLRLRGIFFSHFRDMQNLQDAYENKKPFYLTERGPSSAMHYGHLLIPPIFTKWLQDVENPVPLI 116
I_D	67 RSYFEAHRDENEELLDAYRGGKLYLITRGPSSEAMHYGHLLIPPIFTKWLQDVENPVPLI 126	DB	76 KPHFLRLRGIFVFSHRDLJLILDREYKGEPFLYTRGPSSDSVHGTIPPEFTKWLQD 135
CY	124 QNTDDEXYLWQDLTQDAYDAVENAKDIIACCGDINKTFIFSDLDYGMSSGFYKNTVK 183	QY	117 FNPVLVIMQTDEXYLWQD-LTLDCAYGDAVENAKDIIACCGDINKTFIFSDLDYGMSS 175
I_D	127 QJTDDDEKSIWNLVSVEBQQLAEKAKDIIACAFDVTKTFIFSDFTYTG--GAFYKNTVK 184	DB	136 FDVLVLVIMQTDEXYLFSKERTTBVEVGYSNNAXNDIAIVGFDPNRTFIFSDFTYTG--G 193
CY	184 IOKHVTENQVKGIGFEGFTSDICIGKISFRAQIAAPSFNSPQFPROTDIQLCPACDQ 243	QY	176 GFYKRYVVKLQKHTFNGQKIGFGETSDICIGKISFPAQAPSNSNPEQIFRD--RT 231
I_D	185 VQRCVUTLNKAMG_FGFSCBDPAAKSLPPVQAVSPFSPSSFPHPGKDNLRCIIPCADQ 244	DB	194 AFYKNNVRLSKHHTLQNORAIQFNDSNTGRHFSGSLLGASSWASSPHIFGDESKTV 253
CY	244 DPFYERMTDVAERIGYXPALIHSSTFPALQAJQTRMSADSPPNSIULDTARQIKTKVN 303	QY	232 DIQCLIPCAIDQDPYFRMTDVAEPR-----IGYPKPALLHSTFPALQGAQFTKMSAD 284
I_D	245 DPFYERMTDVAERIGYXPALIHSSTFPALQAJQTRMSADSPPNSIULDTARQIKTKVN 304	DB	254 AIPCHIPCAIDQDPYFRMTDVAEPR-----IGYPKPALLHSTFPALQGAQFTKMSAD 313
QY	304 KHAFSGGRDTIEBHQFGGNCVDSVSPMLTLEDDDKLCETIRKCYTSGAMLTGELKKA 363	QY	285 PNSSFLFDTAKQIKTKVNHFSGGRTTIEHROFGNCVDYDSFEMVLTTEFFLEDDDKL 344
Db	305 RXAFSGGQDSLSKHEFREGANLEDPVPKYLSLEDDSELEHKCYGBGRMLTGEVKKR 364	DB	314 DESAIPMDTPNQIKNKNYKAPEGGKTVVEERKGDTINVDYAVQTCRFFLDEDE 373
Qy	364 LLEVOLPLIAHICARKEYTDIYKEPMTPPKLSEDFQ 401	QY	345 QIREDTYSGAMLTGELKVALIEVCPPLIAEHQARRKEYTDIYKEPMTPPKLSEDFQ 399
Db	365 LTeVLEIVERHRRARAATVDDMVAFLPSPMSFE 402	DB	374 R.RVAYEBSGDMLTGDLKICKELQTYAAFORRKYDDEAVKLFMTRPKWN 428
		RESULT 12	
QIDW3	OBIDW3	PRELIMINARY;	PRT; 632 AA.
AC	OBIDW3;		
DT	01-MAR-2003 (TREMBLref); 23, Created;		
DT	01-MAR-2003 (TREMBLref); 23, Last sequence update)		
DT	01-OCT-2003 (TREMBLref); 25, Last annotation update)		
DE	Probable tryptophan-tRNA ligase.		
GN	Plasmidium falciparum (isolate 3D7).		
CC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
RN	[1] NCBI_TaxID:36329;		
RP	SEQUENCE FROM N.A.		
RA	Harris B., Leonard N., Clark L., Line A., Barron A., Corton C.,		
RA	Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,		
RA	Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;		
RL	Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL844509; CAD2506; 1.		
DR	GO; GO:0005524; F: Ligase binding; IEA.		
DR	GO; GO:0016874; F: Ligase activity; IEA.		
DR	GO; GO:0004830; F: tryptophan-tRNA ligase activity; IEA.		
DR	GO; GO:0006436; P: tryptophan-tRNA aminoacylation; IEA.		
DR	InterPro; IPR002305; tRNA-synt_1b.		
DR	InterPro; IPR02306; tRP_tRNA-synt_1b.		
DR	PRINTS; PR01039; tRNA-SYNTTRP.		
DR	TIGRFAMS; TIGR00233; tTSP; 1.		
KW	Ligase.		
SQ	SEQUENCE 632 AA; 73099 MW; B3E9CE08A4BF0C51 CRC64;		
Query Match Score 48.5%; Best Local Similarity 50.1%; Pred. No. 4.4e-81;	Length 632;		

Matches	203;	Conservative	66;	Mismatches	114;	Indels	22;	Gaps	5;
Qy:	9	EAEEDFEDVWTTQPSAAGKIDYDIDLJVRPFSSKIDDELNIREATGQPFFHFLRGIFF							Best Local Similarity 46.1%; Pred. No. 5e-74;
Qy:	227	ERSKD-VTEWDVNNEE3INNNKLKEFGCSKTKTENHFKRKECTNSKAHHFTRGGIFF							Matches 179; Conservative 76; Mismatches 123; Indels 10; Gaps 3;
Qy:	69	SHDRMNOVLDAYERKRPFLTYTRGPSSSEAMHVGHLIPLFTKWLQDVPNVPLVQMTTD							Qy 12 EDVPDPWTWTSAAK---GIDYDKLIVRGSSKSKIDKELEINRIERATGQPFFHFLRGIF 67
DI:	286	SHRDLFLINYYEHRCKCITYTRGPSSLSMHHLIPLFTKWLQDVPNVPLVQMTTD 128							Db 3 EQRTPDWEVSTDEPVPAIDYDKIINGQCEXKENQALAJRLEKDSGEAHYFRGRV 62
Qy:	129	EKYLW-KOLTLQDARYGDAVENAKDIIACGFDDINKTIPFSDDLGMSGSSFYKQWVKQKH							Qy 68 FSHDRMNOVLDAYEKKPFLTYTRGPSSSEAMHVGHLIPLFTKWLQDVPNVPLVQMTTD 127
Qy:	346	EKLFNQNVSLEYINTLNEVNDIISVSLNPFLTFPNTENAVG---LYPTVLSTHK 402							Db 63 FAHDENLILDEZANRPPFLTYTRGPSSRTMIGHTIFLCKYMODFKIRW-QITD 122
Qy:	188	VTEWQNKKE1RGETSDCTGKISPAIQAPSPRSNSPQLFRRDQCLIPCAIDQDYF							Qy 128 DEKFLWKSRLLEDAYAVGRENKDIVAFCUPKITYIFENVE--ASHBEEERLKLISKI 179
DI:	403	TTLNQSMNVEGFMHSNDNGKISTPSQFAPCPFCQCPNFL-GKNTIPCLVPQDQDYF							Db 64 VTFNQVKG-FGFTPSDCTGKISPAIQAPSPRSNSPQLFRRDQCLIPCAIDQDYF 247
Qy:	248	RMTDVAPRIGKXPALLHSTFPALQGRQTRNSASD-----NSSTFLT 292							Db 180 TNLNEA1KWFQGDMSSN1QGVGPFAKEAPCFSSEFRFSK--GAMCIVPAAVDQDPF 236
Dt:	461	RUSRDIAVKAALPKVPHVHSWPGQCVNSASSTKKRDKGSNSTFDHNSVFLT 520							Qy 249 RMTRDVAPRIGKXPALLHSTFPALQGRQTRNSASD-----NSSTFLT 307
Qy:	293	DTAQKQTKVNKAHAFSGCRDTIEHROFGNCNYDVSPEMLTFLEDDCKLBOIRKOTS							Db 237 RLARDKAZKZLGEKKPSSIVSLPDLK3VNRNSASD-----NSSTFLT 307
DI:	521	DTPEQIKKINKAKTAPSGGTTQHEREGGNLLRDISYQDNEGKNEIGEYKK 580							Qy 188 VTFNQVKG-FGFTPSDCTGKISPAIQAPSPRSNSPQLFRRDQCLIPCAIDQDYF 247
Qy:	353	GAMLTGEUKKJAULOPLIAHQARKEVTDIJKVKEFMPTRKLS 397							Db 180 TNLNEA1KWFQGDMSSN1QGVGPFAKEAPCFSSEFRFSK--GAMCIVPAAVDQDPF 236
Db:	581	GEMLSGEIKKCLIDVLTELVRHQEKCKSLTDEIYSTFFDPNPKPS 625							Qy 368 LQBLIAEHOARRKEVTDIJKVKEFMPTRK 395
Db:	357	IQEFVSVRYQESRKVTDDLRFIDINK 384							Db 357 IQEFVSVRYQESRKVTDDLRFIDINK 384

RESULT 13

Q8SQYS PRELIMINARY; PRT; 385 AA.

ID Q8SQYS AC Q8SQYS; PRELIMINARY; PRT; 385 AA.
ID Q9U1F5 AC Q9U1F5; PRELIMINARY; PRT; 490 AA.
ID Q9U1F5 DT 01-MAY-2000 (TRMBLrel. 13, Created)
ID Q9U1F5 DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
ID Q9U1F5 DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
ID Q9U1F5 DE Tryptophanyl-tRNA synthetase.
ID Q9U1F5 GN ECG11_0530.
ID Q9U1F5 OS Encephalitozoon cuniculi.
ID Q9U1F5 OC Eukaryota: Fungi: Microsporidia: Unikaryonidae; Encephalitozoon.
ID Q9U1F5 NCBI_TaxID=6035;
ID Q9U1F5 OC Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatida; Leishmania.
ID Q9U1F5 OX NCBI_TaxID=5664;
ID Q9U1F5 RN [1]
ID Q9U1F5 RP SEQUENCE FROM N.A.
ID Q9U1F5 RC STRAIN=Friedlin;
ID Q9U1F5 RA Both G., Pohl T., Ivens A.C., Lawson D., Quail M., Rajandream M.A., Chan H.M.,
ID Q9U1F5 RA Barrell B.G.,
ID Q9U1F5 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
ID Q9U1F5 RN [2]
ID Q9U1F5 RP SEQUENCE FROM N.A.
ID Q9U1F5 RC STRAIN=Friedlin;
ID Q9U1F5 RA Both G., Pohl T., Ivens A.C., Lawson D., Quail M., Rajandream M.A., Chan H.M.,
ID Q9U1F5 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
ID Q9U1F5 RN [2]
ID Q9U1F5 RP SEQUENCE FROM N.A.
ID Q9U1F5 RC STRAIN=GB-ML;
ID Q9U1F5 RA GenScope;
ID Q9U1F5 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
ID Q9U1F5 RL SEQUENCE FROM N.A.
ID Q9U1F5 RX MEDLINE: 21576510; PubMed:11719806;
ID Q9U1F5 DR Kacinka M.D., Duprat S., Cornillat E., Mettenier G., Thomarat F.,
ID Q9U1F5 DR Pransier G., Barbe V., Peyretailleade E., Bröttier P., Wincker P.,
ID Q9U1F5 DR Debiau F., El Alaoui H., Peyret P., Saurin M., Gouy M.,
ID Q9U1F5 DR Wessénbach J., Vivares C.P.,
ID Q9U1F5 RT "Genome sequence and gene compaction of the eukaryote parasite
Encephalitozoon cuniculi.";
ID Q9U1F5 RT Nature 414:450-453(2001).
ID Q9U1F5 DR EMBL; AU590450; CAD2593-3.1.;
ID Q9U1F5 DR GO; GO:0005524; F-ATP binding; IEA.
ID Q9U1F5 DR GO; GO:0004830; F-tryptophan-tRNA ligase activity; IEA.
ID Q9U1F5 DR GO; GO:0006436; F-tryptophanyl-tRNA aminoacylation; IEA.
ID Q9U1F5 DR InterPro; IPRO02305; tRNA-synt_1b.
ID Q9U1F5 DR InterPro; IPRO01412; tRNA-synt_1b.
ID Q9U1F5 DR InterPro; IPRO02306; tRNA-synt_1b.
ID Q9U1F5 DR Pfam; PF00579; tRNA-synt_1b_1.
ID Q9U1F5 DR PRINTS; PR01039; TRNA-SYNTHTCP.
ID Q9U1F5 DR PROSITE; PS00178; AA-tRNA-LIGASE_I; 1.
ID Q9U1F5 DR Aminoacyl-tRNA synthetase.
ID Q9U1F5 SQ SEQUENCE 490 AA; 44188_MW; 172C68622C51:D3D CRC64;

Query Match 44.5%; Score 942; DB 5; Length 385;

Best Local Similarity 38.1%; Pred. No. 5e-61;

Matches 173; Conservative 87; Mismatches 129; Indels 65; Gaps 11;

Q: 3 HGFDATEEEDFDPWVTOVSARKGIDYDRLVPRGSKTD-----KLTKTNNKAFFSGCDTIEHROGGNGDWDVF 330
 D: 40 EPRGDAGAEDVTPWVVAKPGQINYDRVLTKAKERMDDQARQEMRDVAKCRGTM 99

Q: 55 -----GQRP-----HHFLRRGIFTFSHRDM 73
 D: 100 TITPSANAEVATPULDWPADMLQANASAMQQPPEALAHIFHRDIAFSRDL 159

Q: 74 NOVLDAYE----NKKPFLYTGRGPSSSEAMHVGHLIPFIFTKWLQDVENTPLVIGMTDD 128
 D: 160 HKGLVDIEASVYTGERSVFLYGRGPAGTMGHVLPFMUJXLYQDFSLPVIZQTDD 219

Q: 129 EKYLMKDUTLQAYGAV- ENAKD1IACGPNKINKPFLPSDLDYMGSSGFKNVVKQ 186
 D: 220 EKFLEDRVPFGAKADELIRSNIKD1IAFNPNPRAHFTFERNTHYMG--DMYPTVRLQR 276

Q: 187 HTENQVKGIGFTSDC1GKISFP1QAAFSFSNSFPQIFR-BRTDIOCLIPCAIDQD 244
 Db 277 SMTGNAVKH1G1TSDNVKGKAFTQARCFSTARRVINGDR-PMCLIPCAIDQD 335

Q: 245 PYFRMRTRDVAAPRIGYKPKALHJSTPPALOGAQTMAS-DPNSS1FLTDTAKQTKVN 303
 D: 336 PPFLVULTRAALLKQLPPALHITKEFLALKSLEHEHMSSAEGVTTLHDIDKOVRKKL- 394

Q: 304 KHAFFSGGRDT1EHRQEGGNCDVDSMPLTEFLDDDCLEQIRKDXTSGAMLTGELKA 363
 D: 395 RRAFSGCATLQMOTGANILELDVAYQYLRFCPDDTLFADVTQYRSGTLSSEVKDL 454

Q: 364 LIE-VLQPLTAHQARRKEYTDEIYKEFMPKRL 396
 D: 455 ADDCTIREVHDWERRATVDDYVVEFCIRDI 488

RESULT 15

Q95295 PRELIMINARY; PRT; 136 AA.
 ID Q95295;
 AC Q95295;

DT 01-FEB-1997 [TREMBLrel. 02; Created]
 DT 01-FEB-1997 [TREMBLrel. 02; Last sequence update]
 DT 01-OCT-2003 [TREMBLrel. 25; Last annotation update]

DE

Tryptophanyl-tRNA synthetase (Fragment).

OS

Sus scrofa (Fig.).

Oc

Eukaryota; Metazoa;

Mammalia; Eutheria;

Chordata;

Craniata;

Vertebrata;

Buteleostomi;

Sus.

[1]

NCBI_TaxID=9623;

RN [1]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Small intestine;

RA

Wintero A.K., Fredholm M., Davies W.;

RT

Library";

RL

Submitted (Jul-1995) to the EMBL/GenBank/DBJ databases.

DR

CAB03585.1;

-

GO

GO:0005524; P:ATP binding; IEA.

D2

GC: GC006336; P:tryptophanyl-tRNA ligase activity; IEA.

D2

InterPro: IPR002305; tRNA-synt_1b.

D2

InterPro: IPR002406; Trp_tRNA-synt_1b.

D2

PFam: PF00579; tRNA-synt_1b; 1.

D1

PRINTS; PRO1039; tRNA-SYNTHRP.

F1

NON-TER 1 1

S2

SEQUENCE 136 AA; 136 AA; 136 AA;

MW: 951F75D1B9CD0617 CRC64;

Query Match

Score 682; DB 6; Length 136;

Best Local Similarity 94.1%; Pred. No. 7.e-52;

Matches 128; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

D2

1 PAIQQAPSFSNSPSPQIIFRDRDQCLIPAIADDQPYFTRDVAIRGYPKPALLHSTEF 270

D2

1 PAIQQAPSFSSSSPQIIFRDRDQCLIPAIADDQPYFTRDVAIRGYPKPALLHSTEF 60

QY 64 RGIFFSHDMNCWQIDAYENKKPFLYLYTGRGPSSSEAMVGHLLIPFIFIKWLQDYPNPLV 123
 DB 73 RGFFESGRDLRIDLDEHGEFFFLYTRGRGPSSSEMLGHMVFIFIKWLQEVFDLVL 132
 QY 124 QMTDDESKYWK-DLTQDAYGDAVENAKDITACGFJNKTFIISDIDYMGNSGFYKNNV 182
 DB 133 ELDDEKFLFKHQLTDVKGFAENAKDITAVGPNENTIFPSDLOYMG-GAFFENVV 195
 QY 183 KIQRHFTFQYQJEGPTFSDCIGKSFPAQAFSNSFSPQIFIDRTDIOCLICAI 242
 DB 191 RTSRQITSTAKAVERGFTSDCIGKHFASITATPSSSEDSLDPKTPCLICAI 250
 QY 243 QDPYPRHTDVAPIRGYKPKALHSTFPALQGAOTKMSASDPNNSIFELDTAKQIKTKV 302
 DB 251 QDPYPRVCVDADORTFKPALHAKFPAQAGASTKMSASDITTSIFMDTAKQIKKI 310
 QY 303 NKHAFASSGGDRDIEHRQFGNCNDVDSFMYLTFLEDDKLQEIRKDYSAMLTGELKK 362
 DB 311 NKYAFASSGGRATAEERHGELQPEVDAFOYLSFPSYDDEKLQAQEQYRGKEILSGEMKK 370
 QY 363 ALIETQPLLAEHQARRKEYTDEIVCFMTPRKCSF 398
 DB 371 ECITVLQEFVSAYQERSKSYDQDVVEKFMRPHKLV 406

RESULT 2
 US-09-348-352-4201
 Sequence 4201, Application US/C332B352
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO: 4201
 LENGTH: 338
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii
 US 09-328-352-4201

Query Match 9.2%; Score 195; DB 4; Length 338;
 matches 84; Conservative 56; Mismatches 139; Indels 46; Gaps 13;

Y 82 NKKPFYLYTGRGPSSSEAMVGHLLIPFIFIKWLQDVPENVPLVI---QMTDDEKYLNWKL 136
 b 6 DORPLIL-TGDRTGQ-LHLGHFVGSLRSRVHQDSSHOOHLJLADQALTNAD----- 57

Y 137 TLDQAYGDAVENAKDITACGFJNKTFI-F--SDIDYMGNSGFYKNNV--VVKIQXHWTNFN 191
 b 58 NPDVKRNLETAHDYLAVGIDPTEKTRICVQSCLPNEMLTINFTVVARLBNPTK 117

Y 192 QVKGIGFTSDCIGKSFPAQAFSNSFSPQIFIDRTDIOCLIPDYPFRMT 250
 D 118 SFIQMRGPERDIPAGFLCYPVQA-----DITAKATVPPVGEQPMLBQT 165

Y 251 RDVAPRIGYK-----KPALHSTFPALOGACTKMSASDPNNSIFELDTAKQIKTK 301
 b 166 NEIVRRVNRIQGDLPECKALLSNMARLPGFDG-KARMSKSLGN-TIVLNASDQDIIKA 223

Y 302 VNKHAFSSGGDRDIEHRQFGNCNDVDSFMYLTFLEDDKLQEIRKDYSAMLTGELK 361
 b 224 VNAMYTDPNHLRILEDPPQVEGN---ITVFTYLDAAEPNKEVEELKHYRGGGLGDGTVK 279

Y 362 KALIEVLQPLLAEHQARRKEYTDE 385
 b 280 KRLEGWVKELEHPIREERELAKD 303

US-09-107-532A-5765
 Sequence 57.65; Application US/09107532A
 Patent No. 658275
 GENERAL INFORMATION:
 APPLICANT: Lynn A. Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS: 7310
 STREET: GENOME THERAPEUTICS CORPORATION
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02434
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Axinielle, Pamela Denekie
 REGISTRATION NUMBER: 40,489
 REFERENCE DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-0277
 INFORMATION FOR SEQ ID NO: 5765:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 348 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1..348
 SEQUENCE DESCRIPTION: SEQ ID NO: 5765:
 US-09-107-532A-5765

Query Match 8.8%; Score 186; DB 4; Length 348;
 Best Local Similarity 24.9%; Pred. No. 4,3e-12;
 Matches 82; Conservative 57; Mismatches 120; Indels 70; Gaps 14;

Qy 88 LYTRGRGPSSSEAMVGHLLIPFIFIKWLQDVPENVPLVQMTDDEKYLNWKL 147
 Db 17 ILTGDRTGK-LHLGHFVGSLKTR-----VANQADEDNOLFWMIAQDQALTNAK 65

Qy 148 N-----ARDIACGFDINKT--FIFSDLDYGMCSGFYKNTV--KIQKHVT-- 189
 Db 66 NPEKVSSSNVLQVADYLAVGLDPAKSTLFIQSOIPELAELIMYLNLVSGVRNRNPTVK 125

Qy 190 --FNOVQGIGFTSDCIGKSFPAQAFSNSFSPQIFIDRTDIOCLIPDYP 246
 Db 126 TELEQKK---FGEVSPTGFETYPVPSQNA-----DITAFAVNLVVGEDQKPM 169

Qy 247 FRMTRD-----VARRIGYKPKALHSTFPALQGQIQTMSASDPNNSIFLTD 293
 Db 170 LEQTOEIVQSNHNTYGEVLFVKEGVPKGMGR--LPGDG-NGKMSKSLGN-3Y1SD 224

Qy 234 TAKQIKTKVNHAFSGGRDTIEHROFGNCNDVDSFMYLTFLEDDKLQEIRKDYS 353
 Db 225 PADVQJKKV---MSMYTDPNHIIQDQVEGRNFTYLDVFGTDEA-ELEMKAHYRRG 280

RESULT 3

Qy 354 AMLTGELKKALIEVQLPLIAEHQARRKEV 382
 Db 281 GLPDVKIRKYLIVLEAEFPAPRARREEL 389

RESULT 4

Sequence 2, Application US/089228100
 Patent No. 6046174

GENERAL INFORMATION:
 APPLICANT: Gentry, Danile
 APPLICANT: Greenwood, Claire
 APPLICANT: Lawlor, Elizabeth
 TITLE OF INVENTION: No. 6046174el trps
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 STATE: PA
 COUNTRY: USA
 ZIP: 19406-0939

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/928,100
 FILING DATE: 12-SEP-1997
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 9619072, 3
 FILING DATE: 12-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gianni, Edward R
 REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P31624-1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4479
 TELEFAX: 610-270-5090
 TELEX:

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 341 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-928-100-2

Query Match Score 8.8%; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 4; 8e-12;
 Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Qy 84 KPFLYTGRGPSEAMHVGHLLIPPEFTKMLQDVFNPLVQMTDDEKY-LWKLDTLDQAY 142
 Db 3 KPIIL-TGDRPTGK-LHIGHVGSKRNR----VLLQEDKVDNFVLAQQAL 49

Qy 143 GDAVEN-----AKDIIACGFDINKTEIF--SDLDYMGMSGFYTKNVV---KIQK 186
 Db 50 TDHADKPQTIVESIGNVALDYAQLDPELAESMYMNLYSTARLER 109

Qy 187 HVTFNQVKGIFGFDSDCTGKISPAQAA--PSFSNSFPQIIFRDRDTCQCLIPCAIDQD 244
 Db 110 NPTVKTEISOKGFESIPIGFLVPIAQARDITAXANY-----VPVGTQDK 156

Qy 245 PYFRMTRD-----VAPRIGYKPKALHSTFPALQAGQTMASDPNSSF 290
 Db 157 PMEQOTREIVRSFNNAYNCVLPVEGIPENE -RAGRLPGLNG-NARMSKS-LNNGLY 212

Qy 291 LTDIAKQIKTKVNHAFSGGRDTIEEHRQFGKCDVDSFMYLFFF--LEDDDKLEQTRK 348

Db 213 LADDATLREKVMMSYTDPHTRPDKLEGN----MVPHYLDFVRPDEAQETADYKE 268
 Qy 349 DYTSGAMLTGEGLKALIEVQLPLIAEHQARRKEYTDEI 386
 Db 269 RYQRGGLGDKTTERKYLELRELGPTRERRIEFAKDM 306

RESULT 5

US-09-492-581-2

Sequence 2, Application US/09492581
 Patent No. 6346449

GENERAL INFORMATION:
 APPLICANT: Greenwood, Claire
 APPLICANT: Lawlor, Elizabeth
 TITLE OF INVENTION: No. 6346409el trps
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 ZIP: 19406-0939

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/492,581
 FILING DATE: 12-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gianni, Edward R
 REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P31624-1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 TELEX:

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 341 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-492-581-2

Query Match Score 8.8%; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 4; 8e-12;
 Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Qy 64 KPFLYTGRGPSEAMHVGHLLIPPEFTKMLQDVFNPLVQMTDDEKY-LWKLDTLDQAY 142
 Db 3 KPIIL-TGDRPTGK-LHIGHVGSKRNR----VLLQEDKVDNFVLAQQAL 49

Qy 143 GDAVEN-----AKDIIACGFDINKTEIF--SDLDYMGMSGFYTKNVV---KIQK 186
 Db 50 TDHADKPQTIVESIGNVALDYAQLDPELAESMYMNLYSTARLER 109

Qy 187 HVTFNQVKGIFGFDSDCTGKISPAQAA--PSFSNSFPQIIFRDRDTCQCLIPCAIDQD 244
 Db 110 NPTVKTEISOKGFESIPIGFLVPIAQARDITAXANY-----VPVGTQDK 156

Qy 245 PYFRMTRD-----VAPRIGYKPKALHSTFPALQAGQTMASDPNSSF 290
 Db 157 PMEQOTREIVRSFNNAYNCVLPVEGIPENE -RAGRLPGLNG-NARMSKS-LNNGLY 212

Qy 291 LTDIAKQIKTKVNHAFSGGRDTIEEHRQFGKCDVDSFMYLFFF--LEDDDKLEQTRK 348

Db 213 LADDATLREKVMMSYTDPHTRPDKLEGN----MVPHYLDFVRPDEAQETADYKE 268
 Qy 349 DYTSGAMLTGEGLKALIEVQLPLIAEHQARRKEYTDEI 386
 Db 269 RYQRGGLGDKTTERKYLELRELGPTRERRIEFAKDM 306

RESULT 6

US-09-492-581-2

Sequence 2, Application US/09492581
 Patent No. 6346449

GENERAL INFORMATION:
 APPLICANT: Greenwood, Claire
 APPLICANT: Lawlor, Elizabeth
 TITLE OF INVENTION: No. 6346409el trps
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 ZIP: 19406-0939

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/492,581
 FILING DATE: 12-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Gianni, Edward R
 REGISTRATION NUMBER: 38,891
 REFERENCE/DOCKET NUMBER: P31624-1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-4478
 TELEFAX: 610-270-5090
 TELEX:

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 341 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-492-581-2

Query Match Score 8.8%; DB 4; Length 341;
 Best Local Similarity 24.0%; Pred. No. 4; 8e-12;
 Matches 81; Conservative 60; Mismatches 128; Indels 69; Gaps 15;

Qy 64 KPFLYTGRGPSEAMHVGHLLIPPEFTKMLQDVFNPLVQMTDDEKY-LWKLDTLDQAY 142
 Db 3 KPIIL-TGDRPTGK-LHIGHVGSKRNR----VLLQEDKVDNFVLAQQAL 49

Qy 143 GDAVEN-----AKDIIACGFDINKTEIF--SDLDYMGMSGFYTKNVV---KIQK 186
 Db 50 TDHADKPQTIVESIGNVALDYAQLDPELAESMYMNLYSTARLER 109

Qy 187 HVTFNQVKGIFGFDSDCTGKISPAQAA--PSFSNSFPQIIFRDRDTCQCLIPCAIDQD 244
 Db 110 NPTVKTEISOKGFESIPIGFLVPIAQARDITAXANY-----VPVGTQDK 156

Qy 245 PYFRMTRD-----VAPRIGYKPKALHSTFPALQAGQTMASDPNSSF 290
 Db 157 PMEQOTREIVRSFNNAYNCVLPVEGIPENE -RAGRLPGLNG-NARMSKS-LNNGLY 212

Qy 291 LTDIAKQIKTKVNHAFSGGRDTIEEHRQFGKCDVDSFMYLFFF--LEDDDKLEQTRK 348

RESULT 6

Sequence 2, Application US/09425666

PATENT NO. 6416976

GENERAL INFORMATION:

APPLICANT: Gentry, Danile
Greenwood, Claire

APPLICANT: Lawlor, Elizabeth

TITLE OF INVENTION: No. 64169761 tips

NUMBER OF SEQUENCES: 6

ADDRESSSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

ZIP: 19406-0939

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEC for Windows Version 2.0

APPLICATION NUMBER: US/09/4225,666

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,100

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Gianni, Edward R.

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P31624-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 341 amino acids

TYPE: amino acid

SPANDENESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-425-666-2

RESULT 7

Sequence 5784, Application US/09134000C

PATENT NO. 6617155

GENERAL INFORMATION:

APPLICANT: Lyne, Doucette-Stamm et al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

PRIOR APPLICATION NUMBER: US/09/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 5784

LENGTH: 335

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-5784

Query Match 8.2%; Score 174; DB 4; Length 335;

Best Local Similarity 23.5%; Pred. No. 9,1e-11;

Matches 81; Conservative 59; Mismatches 123; Indels 82; Gaps 16;

Query 88 LYTGRRGPSSSEAHVGHLLIP-----FIFTKWLQPVENPLVIOMTDDEY 131

Db 5 ILTGDRTGK-LHGHYVGSLKKRVEWQADPTMQLFVMTADLQ-----AIDNAR- 53

Query 132 LWDLTLDDQAYDAVENAARDIIAGFDINKTEIF--SLDYMGMSGGFVKVV--KIQK 186

Db 54 -----NPKEVSAVLEVWLDYLAVGLDPPTKTFIQSQQPQLAEITMYLNLYTSVRY 108

Query 187 HVT----FNQVKGLFGFTDSDCIGKLSKPQIAQAPSNSFPQIQRDTDIQ-LIPCAI 241

Db 109 NPTVKAIEQRK---EGEVPGFGFFYPVSQAA-----DITAFANLVPGE 152

Query 242 DDPYPRFMTRD-----VAPRIGYXPXPAHLISTFPALQAGTQNSASDPNS 288

Db 153 DQPKMLBQAEQEVHSFPNQTYGEVLRBEAVLPKGMR---LPGIDG-NGMNSKSLGN-G 207

Query 289 IFLTDIAKQIKTKVNKEAASGRCRTEBHQFGNCDDVFSMYLTFFLEDDE-EQTRK 348

Db 208 IYLSDPAEVQVKVMSMTPDHPIREDPGQVEGN---MVFYLLDVEGKRNKEYIEBLKE 263

Db 264 HYRHGGLGDDKTKLIDVLDEELAPIRREBELAKNPEA-MEML 308

RESULT 8

Sequence 39, Application US/08743130A

PATENT NO. 5811987

GENERAL INFORMATION:

APPLICANT: Sussanfar, Mandana

APPLICANT: Gallant, Paul L.

APPLICANT: Shen, Xiaoyu

APPLICANT: Tao, Nianjun

APPLICANT: Tao, Jianshi
 APPLICANT: Houman, Fariba
 TITLE OF INVENTION: CANDIDA TYROSYL-tRNA SYNTHETASE PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Mililton Drive
 CITY: Lexington
 STATE: Massachusetts
 ZIP: 02173
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/743,130A
 FILING DATE: 01-NOV-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BROOK BSG., David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: CPI95-12
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEX/FAX: (617) 861-9540
 INFORMATION FOR SEQ ID NO: 39:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 409 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-743-130A-39

Query Match 7.8% Score 164.5; DB 2; Length 409;
 Best Local Similarity 20.7%; Pred. No. 1.5e-09;
 Matches 78; Conservative 59; Mismatches 132; Indels 107; Gaps 16;

Db 76 VLDAYENK-KFPELYTGRRGPSSBAMEVGHLLTPEI-----FTKWLQDY- F 117
 27 IKDVLKEENRFPVKYKGTAPICKP-HGYFVFMKILAHFLFKGCEVILLAHFLDDNN 85

Qy 118 NPLVITQMTDDBKYLKDLTIDQAYDAVENAKDILAGCFINKTFESDLYMGSDF 177
 Db 86 KAPLEVVKYRKYKYEPTVKALKSINVPIERKFGVSSYORGDDYV--MDLFKLNSIV 142

Qy 178 YKNVVK-----LQKHTVFNQYKIGFFTSDCIGKISFPAQAAAPSFSNSNPQIFERDID 232

Db 143 SONDARRAGADVVKQVANPLLGLI-----YPMCA-----IDEHLG 180

Qy 233 IQLIPCALDQPYFMRTRDVAPRIGPKPALHSTFPALQGAQTKMSADPNSSIFLT 292
 Db 181 VDAQFG-GWDRKTFVQDKTIVLAENLPSIGYKRAHLMNPMPGI-GQGGRMSADPNSKIDII 238

Qy 293 DTAKQJKTQKNAFHSGG---RTD-----LEHRQGGN 323
 Db 239 EEPKVVKKKDSATCAPGEKLNDGLIAFIEVYIOPIAELKGVEGAFKCDIDRPEKYG- 297

CY 324 CDVDYSEMYLTFLEDDDKLQEIRKDQTSGAMLTGEKKALI---EVLOPLIAEHQARR 379

Rb 298 ---PSY-----DSIEQLKADEFVDRKLAPPDLKSCVADKINELLARPREFESS- 343

CY 380 KEVTDIEVKEFMTDRK 395
 Rb 344 -----BEFQVAQK 351

RESULT 9
 TS-38-743-130A-2
 Sequence 2, Application US/08743130A
 Patent No. 5871987

RESULT 10
 US-09-489-039A-8660
 ; Sequence 857, Application US/09489039A
 ; Patent No. 6,511,0836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709-2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIORITY APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; LENGTH: 385
 ; TYPE: PRT
 ; ORGANISM: *Klebsiella pneumoniae*
 US-09-489-039A-8660

Query Match
 Best Local Similarity 24.4%; Score 157.5; DB 4; Length 385;
 Matches 87; Conservative 53; Mismatches 142; Indels 75; Gaps 17;

Qy 60 HPERR---GIFFHSDMMNOVLDAYENKK----PFWLYTGRGPSSSEAYHVGHLIPPEIFT 110
 Db 25 HFQSRRKAAVLFVSOR----LSSABQSDKE-SLMNNHEQTIGDRDGTQ-LHHLGYVGSLRQ 78

Qy 111 KWLQDVENVPLVITOMTDEKYLKDQLTDQAYDAVENAK----DIAGCPDI 159
 Db 79 R-----VAIQRHNRHQFILADL--QGLTDGNSPKQSHLFLWMDYAVLNGDT 126

Qy 160 NKTFIF--SDLWGMSSGFYKVNV---KIQKHTFTNQVKIGTFFGKTSDFCIGKISFPAlQ 214
 Db 127 RLTTCICLQALPAELAALSALYKMNIVTVARVERNPVTVKNEIAQKGFAASLSPVGHLAYPISQ 185

Qy 215 ARPSFSNSFPQFLFRDIDQC-LIPCA1DQDPYFRMTRDVA-----PRIGYPKPAl 264
 Db 187 AA-----DTIAFKAEVLPVGDQLEMIEQTNIEVTKHNSLITGEPVIRHKALL 234

Qy 265 LHSTFFFPAQGQTKMSASPDNSVSLFDTAKIXTKVNHAFSGGRDTIEFHFRQFG-G 322
 Db 235 SEVSRUPGVDG-NAKNSXSLGN-TLTISATEB1----HRHVS-AMYTDPPHLRVSDPG 286

Qy 323 NCDVDYFSMLTFLFEDDDKLEQFLQIKRDYTGAMMTGELKKALLEVLOPLIAEHQARR 379
 Db 287 HVEGNVTFTYLLDAFHSDKARVAAEMKTHYQRGGLGDRCKNELETCQLTLLAPIERRR 343

RESULT 11
 US-09-198-452A-857
 ; Sequence 857, Application US/09198452A
 ; GENERAL INFORMATION:
 ; APPLICANT: Grifkaais, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198,452A
 ; CURRENT FILING DATE: 1998-11-24
 ; NUMBER OF SEQ ID NOS: 6849
 ; SEQ ID NO: 857
 ; LENGTH: 344
 ; TYPE: PRT
 ; ORGANISM: *Chlamydia pneumoniae*
 US-09-198-452A-857

Query Match
 Best Local Similarity 23.1%; Score 152; DB 4; Length 344;
 Matches 79; Conservative 50; Mismatches 127; Indels 86; Gaps 16;

MOLECULE TYPE: Peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1184699
US-09-123-615-4

Query Match 6.3%; Score 132.5; DB 3; Length 388;
Best Local Similarity 20.8%; Pred. No. 5.4e-06;
Matches 80; Conservative 58; Mismatches 121; Indels 125; Gaps 20;

Query Match 6.3%; Score 132.5; DB 3; Length 388;
Best Local Similarity 20.8%; Pred. No. 5.4e-06;
Matches 80; Conservative 58; Mismatches 121; Indels 125; Gaps 20;

Qy 91 GRGPS-SEAMEVGHLLPFIFTKQDVENTVPLVYOMTDE--KYLWKLDTLDDQ---AYGD 144
Db 2 GDAPSPEEKH----LITRNLUQEVILGEEKLKEILKEPELKVYTGATTTGKPHVAYFV 54

Qy 145 AVENAKDIIACGSDINKEFISDL-----DYMGMNSGFKYKTYKIQKH---VTF 190
Db 55 PMSKIADEFLKAGCDEV--TILFDLHAYLDNMKAPELLELRVSYTENVIKAMLESIGVPL 112

Qy 191 NQVKGIFG-----FTPSD-----CIGKISFPAIQAA 216
Db 113 EKLEREIKGTDYQLSKEYTLDVYRLSSVVTQHESKXAGAETVKYQEHPILLSGLYPGLQA- 171

Qy 217 PSFSNSFSPQLFRDRDIQCDIPIAIDQDPYRMTEDVAPRIGTPKPALLSTIFFPALOGA 276
Db 172 -LDEEYLVY---DAQF---GGDQDKIFTFAEKYLPALEGSKVHLMMNPVYGLTG- 220

Qy 277 QTKMSASDPNNSIFLTDTAKQIKTKVKNHAF-----SGGRDTEEH----- 317
Db 221 -SRSSESBEESKIDLDLDRGDFDVRKLLK-AFCPEPNVENGVLISFIKHLIFPLSEFVIL 278

Qy 318 -RQFGGNCNDVYNSFPMYLTFFELDDDKLEOIRKDYTSQAMLTGEKKALIEVLQPLIAH 375
Db 279 RDEKRGGN-----KTYTAYVD-----LEQDFAAEVTHPGDLSKNSVEVALNKLL--- 321

Qy 376 QARRKEVTDIYKEFMP--RKLS 397
Db 322 -----DEIREKENTPALKLLA 337

RESULT 13
Sequence 4, Application US/09123615
Patent No. 6090377

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,615
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,868
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: PF-0117 US
REFERENCE DOCKET NUMBER: PF-0117 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

RESULT 14
US-09-543-681A-4257
Sequence 4257, Application US/09543681A
Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709-1.002-005
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO: 4257
LENGTH: 356
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4257

Query Match 5.8%; Score 123; DB 4; Length 356;
Best Local Similarity 23.6%; Pred. No. 5.5e-05;
Matches 86; Conservative 54; Mismatches 142; Indels 82; Gaps 19;

Qy 73 MNQVLDAYENMKPKPFVLYTG---RGPSSSEAMHVGHLIPFTKWLQDVENVPLVYOMTDE 129
Db 18 MNKYLT--ENKS--IVLTDGRIT3-----LHLGHYTGSQCR-WEFQNKRATQYILMADMQ 63

Qy 130 KYLWKLDTLDDQAYGDAVENAKDIIACGSD-----INTKFIPISOLDYGMMSGYKNTYKIQ- 135
Db 59 GLTDNGSTPKVSKELFQDYYADLAVIDDPLSLTCLOQSAPALSELMYLNTTVSRL 128

Qy 196 -----XHVTENQVKGIFFGFTDSDC-GKISFPAIQAA--PSFSNSFSPQLFRDRTDIQCLL 237

Db 129 ERNPVYKHEILQK----NLSRSLPAGFLTYPVSQAADITAPSAD-----IV 170
 Qy 238 PCAAQDPYFPRMTDVAFR---IGYP----KPAALLHSTFPALOGAQCTKMSASDPNES 288
 Db 171 PAGEDEOLMIEBTQEINTEIVTKNSLQGPVLTSCKVVAQVGRPLPGTDGS-GKMKSLGN-T 228
 Qy 289 IFLTDTAKOIKTKYKNGHPSGGRTDIBEHQFGNCNDVDSFMVLTPELEDDDKLEQIRK 343
 Db 229 INIUSSTADEIK---KAVYSMTDPQHIDVAVSPGHIEGNWVFYLDQFCQDKATVYANKA 284
 Qy 349 DNTSGAMLTGELK-KALI----EVLQPL----ISHQARKEKVTDE 385
 Db 285 HYQRGL--GDMKCKAMLNLDIQLLQPTRKXRAQLINDKAYLQVIKEGSDFAKEVTTQ 342
 Qy 386 IVE 389
 Db 343 KLE 346

RESULT 15

US-09-543-681A-6769
 ; Sequence 6769, Application US/09543681A

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI

; FILE REFERENCE: 2709-1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIORITY NUMBER: US 60/1,128,706

; PRIORITY FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 9344

; SEQ ID NO 6769

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-6769

Query Match 5.6%; Score 118; DB 4; Length 349;
 Best Local Similarity 21.0%; Pred. No. 0.0002;

Matches 80; Conservative 46; Mismatches 107; Indels 148; Gaps 20;

Dt 83 KKPFYLYTGRSPSEAMHVGHLIPPIFTKWTQDVENVPLVYOMTDEKYLW----KDLT 137

Qy 17 QKPI-VFSGHQPSGE-LTIGMYGAI-RQW-----VQMNDYDCYCIVNDQHAI 63

Dt 138 LDQAYGDAVENAKD---IIACGFDLINKTFPSLDYMGMSGFYKVVVKIQRHVT---- 189

Qy 64 VRQDPTELRKRLDTLALYLAQGIDPEKSTF-----VQSHVPQHAQ 105

Dt 190 -----FNQVKGIFGFTDSDC-----IGKISFPAIQAPSFNSNFSFPOQIFDRDRTD 232

Qy 106 LGNNALNCYTGELSRMTQPKDSARHAENINAQFLDYPVLMAA-----DILLYQTN 157

Dt 233 IQCLIPCAIDQDPYPRMTDVAFRIG---YPKPAALLHSTFP-----ALQGATQKMSAS 283

Qy 158 ---QPVVGIDQKQHIELSRIAQERNIAQDIFTYPDPF-LKG3ARVMALQDEARKMSKS 214

Dt 284 DPNSS---IFLTD---TAKOIKTKY-----NKEAEG-----GRDTI 314

Qy 215 DDNRNNVIALLEDPKAAAXXIKRAVTDSEEPVRYADLENKAGTSNLDDLAGYTGKTIP 274

Dt 315 EEEHQFGGNCDDVDSFPMVLTPELEDDDKLEQIRKDYTSGAMLTBGLKLJIEVQPLIAE 374

Qy 275 ELEAEFEQK-----MY-----CHIKGAAVAAEVSMDLTN 302

Dt 375 HQAR----RKEYTDEIVKE 389

Qy 303 IQSERFNTFRNDEALINKIME 323

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OM protein - protein search, using sw model

Run on: August 24, 2004, 17:18:04 ; Search time 126 Seconds

(without alignments)
 899.219 Million cell updates/secTitle: US-09-813-718-10_COPY_71_471
 Perfect score: 2116

Sequence: 1 SNHGPDATAEEDFVDPPNV.....VTDEIVKEFMTPKLSEFDQ 401

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_29Jan04:*
- 2: geneseq1980s:*
- 3: geneseq2000s:*
- 4: geneseq2001s:*
- 5: geneseq2002s:*
- 6: geneseq2003as:*
- 7: geneseq2003os:*
- 8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query

Match

Length

DB

ID

Description

1	2116	100.0	401	5	AAG79549	Aag79549 TrPRS T1
2	2116	100.0	415	4	AAB47617	Aab47617 Human sup
3	2116	100.0	415	5	AAE13493	Aae13493 Human sup
4	2116	100.0	415	5	AAG79548	Aag79548 His6-tag
5	2116	100.0	415	6	ABU72386	Abu72386 Human sup
6	2116	100.0	437	4	AAB47616	Aab47616 Human min
7	2116	100.0	437	5	AAE13492	Aae13492 Human min
8	2116	100.0	437	5	AAG79547	Aag79547 His6-tag
9	2116	100.0	437	6	ABU72385	Abu72385 Human min
10	2116	100.0	484	4	AAB47615	Aab47615 Human full
11	2116	100.0	484	5	AAE13491	Aae13491 Human full
12	2116	100.0	484	5	AAG79546	Aag79546 Full length
13	2116	100.0	484	6	ABU72384	Abu72384 Human full
14	2101	99.3	471	7	ADB25762	Ade25762 Human pro
15	2101	99.3	471	8	ADE76998	Ade76998 Human pro
16	2101	99.3	475	3	AAB58220	Aab58220 Lung carc
17	2096	99.1	471	2	AAV05372	Aay05372 Human HCM
18	1988	94.0	378	5	AAG79541	Aag79541 TrPRS T2
19	1388	94.0	392	4	AAB47618	Aab47618 Human lca
20	1988	94.0	392	5	AAE13494	Aae13494 Human ins
21	1988	94.0	392	5	AAG79544	Aag79544 His6-tag
22	1988	94.0	392	6	ABU72387	Abu72387 Human min
23	1973	93.2	378	6	AAG79953	Aag79953 T2-TrPRS
24	1938	91.6	475	7	ADB79825	Adb79825 Mouse put
25	1370	64.8	450	4	ABB64621	Abb64621 Drosophil

Homo sapiens

OS

XX

PN

XX

XX

XX

Schimmel P, Wakasugi K, Friedlander M;

XX

XX

XX

WPI: 2002-698635/75.

Example 1; Page 78-79; 83pp; English.

XX

This sequence represents a novel cleavage product, T1, of recombinant human tryptophanyl-tRNA synthetase (TrPRS), a related cleavage product, T2, is water soluble and comprises residues 94-471 of full length TrPRS. The water-soluble T2 polypeptide is useful for inhibiting ocular neovascularization in a patient. The T2 polypeptide is useful for treating neovascularization, e.g. rubrotic glaucoma, retinopathy, keratitis, or pterygia.

XX

PT

PT

ALIGNMENTS

26	1370	5	64.8	430	4	ABB67203
27	1304	61.6	402	3	AAG23698	Drosophili
28	1218	57.6	426	3	AAG23697	Arabidops
29	1200	55.7	424	5	AAB66931	Arabidops
30	1163	55.0	424	5	ABP73795	Tryptophana
31	1125	53.2	432	6	Abr3898	Candida a
32	1107	52.3	433	6	ABJ26487	Protein S
33	1107	52.3	456	7	ADB70160	Aspergilli
34	988	45.7	292	3	AAB3695	C. neoform
35	801	39.3	173	3	AAB8517	Arabidops
36	803	37.9	385	4	AAB86409	Lung canc
37	414	19.6	179	6	Abj5887	Putative
38	328	15.5	85	5	AEE13515	Human try
39	328	15.5	85	6	ABU2416	Abu2416
40	292	13.8	85	6	ABU2417	Bovine tr
41	273	12.9	85	6	ABU72419	Abu2419 Rabbit tr
42	263	12.4	85	6	ABU72418	Abu2418 Mouse tr
43	226	5.5	142	3	AAB56219	Abu2419 Lung canc
44	203	5.5	341	5	ABP26564	Streptoco
45	195	9.2	337	6	ABU17282	Protein e

CC prematurity; keratitis; ischaemic retinopathy (e.g. sickle cell),
 CC pathological myopic; ocular histoplasmosis, pterygia, or punica;
 CC innerchoriopathy. This polypeptide is particularly useful for treating
 CC retinal degeneration to prevent the damaging effects of trophic and
 CC growth factors, and for promoting vascularisation to retard retinal
 CC degeneration by enhancing blood flow to cells. These are also useful for
 CC regulating vascular endothelial cell function, and in particular, for
 CC inhibiting angiogenesis.

Sequence 401 AA:

Query Match Score 100.0%; Pred. No. 1e-209; Length 401;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 401; Conservative 0;

Qy	1 SNGHPDATEAEDFDVDEWTVQTS	SAKGIDYDKLIVRGSSKIDKELINRIBERATGORPHH	60
Db	1 SNGHPDATEAEDFDVDEWTVQTS	SAKGIDYDKLIVRGSSKIDKELINRIBERATGORPHH	60
2Y	61 FLURGIFFFSHRDMMQVLDAYENKKPPLTLYTRGPSSRAAMHYGHLLIPIFTKQI	QDFENVP	120
2b	61 FLURGIFFFSHRDMMQVLDAYENKKPPLTLYTRGPSSRAAMHYGHLLIPIFTKQI	QDFENVP	120
2Y	121 LVIQMTDDEKYLKDULDQAYDAVENAKOIIACGFIDINKTFIFSDLYDGMSSGYKN	180	
2b	121 LVIQMTDDEKYLKDULDQAYDAVENAKOIIACGFIDINKTFIFSDLYDGMSSGYKN	180	
2Y	181 VVKIKQRHVNQVKGIFGGFTDSDCIGKISPAIQAPSFSNSFPQLFRDIDICLIPCA	240	
2b	181 VVKIKQRHVNQVKGIFGGFTDSDCIGKISPAIQAPSFSNSFPQLFRDIDICLIPCA	240	
2Y	241 IDQDDYFRTMTRDVAIRGYPKPAHLSTFFPALQAGQTKMSASDPNNSSIFTDTAKQIKT	300	
2b	241 IDQDDYFRTMTRDVAIRGYPKPAHLSTFFPALQAGQTKMSASDPNNSSIFTDTAKQIKT	300	
2Y	301 KVNHKAIFSGGRDTEEEHROFGCNCDYDVSMYLTFLEDDDKLBOIRKOYTSGAMLTGEL	360	
2b	301 KVNHKAIFSGGRDTEEEHROFGCNCDYDVSMYLTFLEDDDKLBOIRKOYTSGAMLTGEL	360	
2Y	361 KKALIEVLOPLIAHQARKEVTEDEIVKEFMTPKLSPDFQ	401	
2b	361 KKALIEVLOPLIAHQARKEVTEDEIVKEFMTPKLSPDFQ	401	

RESULT 2

D AAB47617 standard; protein: 415 AA.
 IX AAB47617;

CX 07-JAN-2002 (first entry)

XX Human supermini TrpRS.

XX Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain;
 XX vascular endothelial cell function; burn; plastic surgery; abdomen;
 XX polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis;
 XX dermal ulcer; diabetic ulcer; endothelialization;
 XX trypopharyl-tRNA synthetase; solid tumour; wound healing;
 XX vascular graft surgery.

XX Homo sapiens.

XX WC200174841-A1.

XX 11-OCT-2001.

XX 21-MAR-2001; 20001WO-US0089966.

XX 31-MAR-2000; 2000CUS-0193471P.
 XX (SCRI) SCRIPPS RES INST.

PI Schimmeil P, Wakasugi K;

XX DR WPI; 2001-626377/72.
 XX N-PSDB; AAH4364.

XX New human truncated tyrosyl-tRNA synthetase polypeptide for regulating angiogenesis; vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction.

XX Disclosure: Page 129-30; 150PP; English.

XX The sequences given in AAB47615-18 show full length and truncated versions of tryptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel.

XX Sequence 415 AA;

Query Match Score 100.0%; Pred. No. 1e-209; Length 415;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy	1 SNGHPDATEAEDFDVDEWTVQTS	SAKGIDYDKLIVRGSSKIDKELINRIBERATGORPHH	60
Db	1 SNGHPDATEAEDFDVDEWTVQTS	SAKGIDYDKLIVRGSSKIDKELINRIBERATGORPHH	60
2Y	61 FLURGIFFFSHRDMMQVLDAYENKKPPLTLYTRGPSSRAAMHYGHLLIPIFTKQI	QDFENVP	120
2b	61 FLURGIFFFSHRDMMQVLDAYENKKPPLTLYTRGPSSRAAMHYGHLLIPIFTKQI	QDFENVP	120
2Y	121 LVIQMTDDEKYLKDULDQAYDAVENAKOIIACGFIDINKTFIFSDLYDGMSSGYKN	180	
2b	121 LVIQMTDDEKYLKDULDQAYDAVENAKOIIACGFIDINKTFIFSDLYDGMSSGYKN	180	
2Y	181 VVKIKQRHVNQVKGIFGGFTDSDCIGKISPAIQAPSFSNSFPQLFRDIDICLIPCA	240	
2b	181 VVKIKQRHVNQVKGIFGGFTDSDCIGKISPAIQAPSFSNSFPQLFRDIDICLIPCA	240	
2Y	241 IDQDDYFRTMTRDVAIRGYPKPAHLSTFFPALQAGQTKMSASDPNNSSIFTDTAKQIKT	300	
2b	241 IDQDDYFRTMTRDVAIRGYPKPAHLSTFFPALQAGQTKMSASDPNNSSIFTDTAKQIKT	300	
2Y	301 KVNHKAIFSGGRDTEEEHROFGCNCDYDVSMYLTFLEDDDKLBOIRKOYTSGAMLTGEL	360	
2b	301 KVNHKAIFSGGRDTEEEHROFGCNCDYDVSMYLTFLEDDDKLBOIRKOYTSGAMLTGEL	360	
2Y	361 KKALIEVLOPLIAHQARKEVTEDEIVKEFMTPKLSPDFQ	401	
2b	361 KKALIEVLOPLIAHQARKEVTEDEIVKEFMTPKLSPDFQ	401	

Qy	1 SNGHPDATEAEDFDVDEWTVQTS	SAKGIDYDKLIVRGSSKIDKELINRIBERATGORPHH	60
Db	2 SNGHPDATEAEDFDVDEWTVQTS	SAKGIDYDKLIVRGSSKIDKELINRIBERATGORPHH	60
2Y	61 FLURGIFFFSHRDMMQVLDAYENKKPPLTLYTRGPSSRAAMHYGHLLIPIFTKQI	QDFENVP	120
2b	62 FLURGIFFFSHRDMMQVLDAYENKKPPLTLYTRGPSSRAAMHYGHLLIPIFTKQI	QDFENVP	120
2Y	121 LVIQMTDDEKYLKDULDQAYDAVENAKOIIACGFIDINKTFIFSDLYDGMSSGYKN	180	
2b	122 LVIQMTDDEKYLKDULDQAYDAVENAKOIIACGFIDINKTFIFSDLYDGMSSGYKN	180	
2Y	181 VVKIKQRHVNQVKGIFGGFTDSDCIGKISPAIQAPSFSNSFPQLFRDIDICLIPCA	240	
2b	182 VVKIKQRHVNQVKGIFGGFTDSDCIGKISPAIQAPSFSNSFPQLFRDIDICLIPCA	240	
2Y	241 IDQDPYFRTMTRDVAIRGYPKPAHLSTFFPALQAGQTKMSASDPNNSSIFTDTAKQIKT	300	
2b	242 IDQDPYFRTMTRDVAIRGYPKPAHLSTFFPALQAGQTKMSASDPNNSSIFTDTAKQIKT	300	
2Y	301 KVNHAFSSGRDTEEEHROFGCNCDYDVSMYLTFLEDDDKLBOIRKOYTSGAMLTGEL	360	
2b	302 KVNHAFSSGRDTEEEHROFGCNCDYDVSMYLTFLEDDDKLBOIRKOYTSGAMLTGEL	360	
2Y	361 KVAKLIEVLOPLIAHQARKEVTEDEIVKEFMTPKLSPDFQ	401	
2b	362 KVAKLIEVLOPLIAHQARKEVTEDEIVKEFMTPKLSPDFQ	401	

RESLT 3
 AAE13493 standard; protein: 415 AA.
 XX ID AAE13493;
 AC XX DT 12-FEB-2002 (first entry)

DE	Human supernuini tryptophanyl t-RNA synthetase in PET20B.	Db	62 FLRRGIFFSHRDMNQVQLDAYENKCFPFYLYTERGPSSEAHVGHLIPFIFTKWLQDVFNVP 121
XX	Human; tryptophanyl-t-RNA synthetase; TrprS; tyrosyl t-RNA synthetase;	CY	121 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 180
KW	TyrrS; vascular endothelial cell function; pressure sore; venous ulcer; injury;	Db	122 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
KW	re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;	CY	123 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
KW	diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;	Db	124 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
KW	angiography; gene therapy; tumour; inflammation; vascular permeability;	CY	125 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
KW	rheumatoid arthritis; psoriasis; diabetic retinopathy.	Db	126 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	Homo sapiens.	CY	127 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	WO203175078-A1.	Db	128 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	11-OCT-2001.	CY	129 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	21-MAR-2001; 2001WO-US008975.	Db	130 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	31-MAR-2000; 2000US-0193471P.	CY	131 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	(SCRI) SCRIPPS RES INST.	Db	132 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IA	Schimmel P, Wakasugi K;	CY	133 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IA	IR WPI; 2002-010784/01.	Db	134 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IR	N-PSDB; AAD22484.	CY	135 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of	RESULT 4	136 LVQIQTIDDKYKLWDLTLQAYDAVENAKDIIAGFDINKTFISDLDYGMSSGFYKVN 181
IX	regulating vascular endothelial cell function, preferably angiogenesis,	ID	AGC79548 standard; protein: 415 AA.
IX	is useful for treating solid tumor or suppressing tumor metastasis in	AC	AGC79548;
ET	mammal.	DT	10-DEC-2002 (first entry)
PT		XX	
XX	Example 1; Page 129-130; 149pp; English.	DE	His6-tagged TrprS T1 polypeptide.
XX	The patent discloses human aminoacyl tRNA synthetases, particularly	XX	T2; tryptophanyl-tRNA synthetase; TrprS; ocular neovascularisation;
CC	truncated tryptophanyl-tRNA synthetases (TrprS) comprising a Rossmann	XW	neovascular eye disease; age-related macular degeneration;
CC	fold nucleotide binding domain and polynucleotides encoding them. The	XW	ocular complication; diabetes; rubetoic glaucoma; retinopathy;
CC	invention also relates to tyrosyl t-RNA synthetases (TyrrS). TrprS	XW	prematuity; keratopathy; sickle cell;
CC	sequences are useful for regulating vascular endothelial cell function,	XW	pathological myopia; ocular histoplasmosis; pterygia; Tis;
CC	preferably angiogenesis. Angiogenic TrprS sequences are useful as wound	XW	punitate innerchoriopath; retinal degeneration; Growth Factor;
CC	healing agents for re-vascularising damaged tissues. They are useful for	XW	vascularisation; vascular endothelial cell function; angiogenesis.
CC	treating full-thickness wounds (e.g. dermal ulcers, including pressure	OS	
CC	sores, venous ulcers and diabetic ulcers), burns and injuries. TrprS	OS	Homo sapiens.
CC	sequences can also be used in plastic surgery when reconstruction is	XX	WO200267970-A1.
CC	required following a burn, other trauma, or even for cosmetic purposes.	XX	06-SEP-2002.
CC	Angiogenic TrprS is also used in association with surgery and following	XX	22-FEB-2002; 2002WO-US005185.
CC	the repair of cuts, for promoting endothelialisation in vascular graft	XX	23-FEB-2001; 2001US-0270951P.
CC	surgery and for repairing the damage of myocardial infarction and in	PA	(SCRI) SCRIPPS RES INST.
CC	conjunction with coronary bypass surgery by stimulating the growth of	XX	Schimmel P, Wakasugi K, Friedlander M;
CC	transplanted tissue. TrprS is also used in conjunction with angiography.	XX	WPI; 2002-69B635/75.
CC	TrprS DNAs are useful in gene therapy. TrprS antibodies are used in	DR	X-PSDB; ABA00330.
CC	immunoassays to detect the presence of tumours. They are also useful for	XX	New polypeptides derived from human tryptophanyl-tRNA synthetase, useful
CC	blocking endogenous angiogenic activity and retard the growth of solid	PT	for inhibiting ocular neovascularization in a patient, or for treating
CC	tumours. These antibodies may also be used to treat inflammation caused	PT	neovascular eye diseases, e.g. rubetoic glaucoma, retinopathy, keratitis,
CC	by increased vascular permeability. Inhibiting the activity of TrprS by	PT	or pterygia.
CC	antisense technology is useful for preventing further growth or even	XX	XX
CC	regressing solid tumours, and for treating rheumatoid arthritis, psoriasis,	PS	Example 1; Page 71-72; 83pp; English.
CC	diabetic retinopathy, all of which are characterised by abnormal	XX	This sequence represents a His6-tagged cleavage product, T1, of
CC	angiogenesis. The present sequence is human truncated tryptophanyl t-RNA	CC	recombinant human tryptophanyl-tRNA synthetase (TrprS). A related cleavage
CC	synthetase. The water-soluble T2 polypeptide is useful for inhibiting	CC	product, T2, is water soluble and comprises residues 94-471 of full
CC	ocular neovascularisation in a patient. The T2 polypeptide is useful for	CC	treating neovascular eye diseases, e.g. age-related macular degeneration,
CC	ocular complications of diabetes, rubetoic glaucoma, retinopathy of	CC	prematuity, keratitis, ischaemic retinopathy (e.g. sickle cell),
CC	protein) in PET20B	XX	
SQ	sequence 415 AA;		
Query Match	Score 2116; DB 5; Length 415;		
Best Local Similarity	100.0%; Pred. No. 1.1e-209;		
Matches	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CC	1 SNHGPDDATEABEDYDFDPWTQTSXAXGIDYDKLIVRGSSSKIDKELINRERATGCRPHH 60		
CC	2 SNHGPDDATEABEDYDFDPWTQTSXAXGIDYDKLIVRGSSSKIDKELINRERATGCRPHH 61		
CC	61 FLRRGIFFSHRDMNQVQLDAYENKCFPFYLYTERGPSSEAHVGHLIPFIFTKWLQDVFNVP 120		

C1 Pathological myopic, ocular histoplasmosis, pterygia, or punctate innerchoroidalopathy. This polypeptide is particularly useful for treating C1 retinal degeneration to prevent the damaging effects of trophic and C1 growth factors, and for promoting vascularisation to retard retinal C1 degeneration by enhancing blood flow to cells. These are also useful for C1 regulating vascular endothelial cell function, and in particular, for C1 inhibiting angiogenesis.

X1 Sequence 415 AA;

Query Match 100.0%; Score 2116; DB 5; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.1e-209; Mismatches 0; Indels 0; Gaps 0;

C/ 1 SNHGDATEAEEDFDPW1QTSQSSAKGIDYDKLIVRGSSKIDKELINERATRQPRHH 60
D/ 2 SNHGDATEAEEDFDPW1QTSQSSAKGIDYDKLIVRGSSKIDKELINERATRQPRHH 61
Q/ 61 FLRGIGPFSSHDMQVLDAYENKECPFLYLTGRGPSEAMHGHILIPETITKMLQDVFNYP 120
D/ 62 FLRGIGPFSSHDMQVLDAYENKECPFLYLTGRGPSEAMHGHILIPETITKMLQDVFNYP 121
Qy 121 LVYOMTDDKYLKDDLQAYDAVENARDIACTAGFDINKTFIFSDLDYMGSSGFYKN 180
Db 122 LVYOMTDDKYLKDDLQAYDAVENARDIACTAGFDINKTFIFSDLDYMGSSGFYKN 181
Qy 181 VVKIQKHYTFENQKVGIEGTDSOOGKTSFPAIQAAPSSNSNFFQIERTDQCLIPCA 240
Db 182 VVKIQKHYTFENQKVGIEGTDSOOGKTSFPAIQAAPSSNSNFFQIERTDQCLIPCA 241
Qy 241 IDQDPYFEMTRDVAPIRGPKPALKHSTPPALQGAQTPMSAQPNSSFLTDIAKQIKT 300
Db 242 IDQDPYFEMTRDVAPIRGPKPALKHSTPPALQGAQTPMSAQPNSSFLTDIAKQIKT 301
Qy 301 KVKHAFGGDRDTEEHQFGNCVDVSFMYLTFFLEDDKLEQIRKDYSQSAMLTQEL 360
Db 302 KVKHAFGGDRDTEEHQFGNCVDVSFMYLTFFLEDDKLEQIRKDYSQSAMLTQEL 361
Qy 361 KKLIAEVQLPLIAHQARKEKNDTEVKEFMRKLISSDFQ 401
Db 362 KKLIAEVQLPLIAHQARKEKNDTEVKEFMRKLISSDFQ 402

RESULT 5
ID ABU72386 standard; protein; 415 AA.

XX ABU72386;
XX DT 16-JUN-2003 (first entry)

Human supermini tryptophanyl tRNA synthetase/Ris tag.

XX Human; tryptophanyl tRNA synthetase; TrPRS; angiogenesis; cytosstatic; vascular endothelial cell; solid tumour; myocardial infarction; enzyme; endotheelial monocyte-activating polypeptide II; tumour metastasis; wound healing; dermal ulcer; endothelialisation; vascular graft surgery; abdominal wound; coronary bypass surgery; gene therapy.
Homo sapiens.
Synthetic.

XX US2002182666-A1.
XO 05-DEC-2002.
XO 21-MAR-2001; 2001US-00813718.

XX PI PT 21-MAR-2001; 2001US-00813718.
XO P1 (SCHI/) SCHIMMEL P.
XO (WAKA/) WAKASUGI K.

XX Schimmel P., Wakasugi K.;
XX WPI; 2003-340974/32.
DR N-PSDB; ACA64107.
XX

XX New truncated tryptophanyl-tRNA synthetase polypeptide comprising a truncated Rossmann fold nucleotide binding domain or having chemokine activity useful for e.g. for regulating angiogenesis and for treating myocardial infarction.

XX Example 1; Page 50-51; 91FP; English.

XX The invention relates to an isolated polypeptide comprising a truncated tryptophanyl-tRNA synthetase (TrPRS); polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity. The isolated polypeptide is capable of regulating vascular endothelial cell function.

XX TrPRS has a C-terminal domain containing an BMP II, endothelial monocyte-activating polypeptide II, a proinflammatory cytokine-like domain and is similar in sequence to TrRS. Also included are a polyimide-oxide encoding TrPRS (or a polynucleotide 95% similar to it), a TrPRS epitope, 5, and 3' deletions of the TrPRS polynucleotide, a recombinant vector comprising an isolated TrPRS nucleic acid, a recombinant host cell containing the TrPRS nucleic acid and expressing TrPRS, an isolated anti-TrPRS antibody, producing angiogenesis by treating it with a protease, and suppressing angiogenesis. TrPRS truncated by treating it with a protease, and suppressing angiogenesis, solid tumours or a condition that would benefit from decreased angiogenesis in a mammal by administering to the mammal the composition comprising the TrPRS truncated protein. The isolated polypeptide is useful for the preparation of a pharmaceutical composition for transdermal, transmucosal, enteral or parenteral administration. The truncated tRNA synthetase polypeptide is useful for research, diagnostic, prognostic and therapeutic applications. The tRNA synthetase are useful for regulating vascular endothelial cell function, particularly for regulating angiogenesis, for treating myocardial infarction and solid tumour, and for suppressing tumour metastasis. Angiogenic tRNA synthetase polypeptides are useful as wound healing agents or for treating full thickness wounds such as dermal ulcers, in the promotion of abdominal wallisation in vascular graft surgery, in the treatment of abdominal wounds where there is a high risk infection, in conjunction with coronary bypass surgery by stimulating the growth of the transplanted tissue, and in gene therapy. The present sequence is a Trp tRNA synthetase protein (full length, truncated or mutant) with a His affinity tag.

XX Sequence 415 AA;

XX Query Match: 100.0%; Score 2116; DB 6; Length 415;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-209; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNEGDPDATEAEEDFDPW1QTSQSSAKGIDYDKLIVRGSSKIDKELINERATRQPRHH 60
Db 2 SNEGDPDATEAEEDFDPW1QTSQSSAKGIDYDKLIVRGSSKIDKELINERATRQPRHH 61
Qy 61 FLRGIGPFSSHDMQVLDAYENKECPFLYLTGRGPSEAMHGHILIPETITKMLQDVFNYP 120
Db 62 FLRGIGPFSSHDMQVLDAYENKECPFLYLTGRGPSEAMHGHILIPETITKMLQDVFNYP 121
Qy 121 LVYOMTDDKYLKDDLQAYDAVENARDIACTAGFDINKTFIFSDLDYMGSSGFYKN 180
Db 122 LVYOMTDDKYLKDDLQAYDAVENARDIACTAGFDINKTFIFSDLDYMGSSGFYKN 181
Qy 181 VVKIQKHYTFENQKVGIEGTDSOOGKTSFPAIQAAPSSNSNFFQIERTDQCLIPCA 240
Db 182 VVKIQKHYTFENQKVGIEGTDSOOGKTSFPAIQAAPSSNSNFFQIERTDQCLIPCA 241
Qy 241 IDQDPYFEMTRDVAPIRGPKPALKHSTPPALQGAQTPMSAQPNSSFLTDIAKQIKT 300
Db 242 IDQDPYFEMTRDVAPIRGPKPALKHSTPPALQGAQTPMSAQPNSSFLTDIAKQIKT 301
Qy 301 KVKHAFGGDRDTEEHQFGNCVDVSFMYLTFFLEDDKLEQIRKDYSQSAMLTQEL 360
Db 302 KVKHAFGGDRDTEEHQFGNCVDVSFMYLTFFLEDDKLEQIRKDYSQSAMLTQEL 361

Qy 361 KKLIAEVQLPLIAHQARKEKNDTEVKEFMRKLISSDFQ 401
Db 362 KKLIAEVQLPLIAHQARKEKNDTEVKEFMRKLISSDFQ 402

Db	24	SNGGDATAEEDFDVDPWVQTSQAKGIDYDKLIVEFGSSKIDKELENRERATGORPHH	83
Qy	61	FLRRGIFSHRDNNQVLDAYENKKPFYLYTGRGPSSSEAMHGHLIPFIFTKMLQDVNVP	120
Db	84	FLRRGIFSHRDNNQVLDAYENKKPFYLYTGRGPSSSEAMHGHLIPFIFTKMLQDVNVP	143
Qy	121	LVIQMTDDEKLKDLTDAYDAVENARDIITAGFDINKTFIFSDLDGMSSGGYKN	180
Db	144	LVIQMTDDEKLKDLTDAYDAVENARDIITAGFDINKTFIFSDLDGMSSGGYRN	203
Qy	181	VVICLQRKHFTFNQVKIGIIGFTDSDCIGKISPAIQAOAPSFSNSFPQLFRDTDIOLCPA	240
Db	204	VVKQKHFTFNQVKIGIIGFTDSDCIGKISPAIQAOAPSFSNSFPQLFRDTDIOLCPA	263
Qy	241	IDQDPYFMRTRDVAPRIGYPKPALLSTTEPALQGAQTMSASDPSNSFIFTDTAQIKT	300
Db	264	IDQDPYFMRTRDVAPRIGYPKPALLSTTEPALQGAQTMSASDPSNSFIFTDTAQIKT	323
Qy	301	KDKHAFSSGRDTIEHRQFGNCDDVSPFMYLTFLEDDDKLEQIRKDYSGAMITGEL	360
Db	324	KDKHAFSSGRDTIEHRQFGNCDDVSPFMYLTFLEDDDKLEQIRKDYSGAMITGEL	383
Qy	361	KKALIEVLOPLAEHQARRKEVTDIEVKREMTPKLSPFDFQ	401
Db	384	KKALIEVLOPLAEHQARRKEVTDIEVKREMTPKLSPFDFQ	424
RESULT 7			
ID AAE13492 standard; protein: 437 AA.			
AC AAE13492;			
DT 12-FEB-2002 (first entry)			
DE Human mini tryptophanyl-tRNA synthetase in PET20B.			
XX Human; tryptophanyl-tRNA synthetase; TRPRS; tyrosyl t-RNA synthetase;			
XX TyrRS; vascular endothelial cell function; angiogenesis; wound healing;			
XX re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;			
XX diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;			
XX angiopathy; gene therapy; tumour; inflammation; rheumatoid arthritis; psoriasis; vascular permeability; diabetic retinopathy.			
OS Homo sapiens.			
XX PN WO200175078-A1.			
XX PD 11-OCT-2001.			
XX PP 21-MAR-2001; 2001WC-US008975.			
XX PR 31-MAR-2000; 2000US-3193471P.			
XX PA (SCRI) SCRIPPS RES INST.			
XX PI Schimmel P, Wakasugi K;			
XX DR WPI-2002-010764/01.			
XX DR N-PSDB; ADD22483.			
XX PT Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in mammal.			
XX PT Sequence 437 AA;			
PS Example 1; Page 123-124; 149pp; English.			
XX The patent discloses human aminocyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (Trprs) comprising a Rossmann fold nucleotide binding domain and Polynucleotides encoding them. The invention also relates to tyrosyl t-RNA synthetases (Tyrs). Trprs sequences are useful for regulating vascular endothelial cell function.			
CC Sequence 437 AA;			
PS Query Match 100.0%; Score 2116; DB 4; Length 437;			
PS Best Local Similarity 100.0%; Pred. No. 1..2e-209; Mismatches 0; Indels 0; Gaps 0;			
PS Matches 401; Conservative 0; Gaps 0;			
PS 1 SNGGDATAEEDFDVDPWVQTSQAKGIDYDKLIVEFGSSKIDKELENRERATGORPHH 60			

Qy 361 KHALIEVQPLIAHQARRKEYTDEIVKEFMMTPRKLSDFQ 401
 Db 384 KHALIEVQPLIAHQARRKEYTDEIVKEFMMTPRKLSDFQ 424

RESULT 9

ABU72285 ID ABU72385 standard; protein; 437 AA.

XX AC ABU72385;

XX DT 16-JUN-2003 (first entry)

XX Human mini tryptophanyl tRNA synthetase/His tag.

DE Human; tryptophanyl tRNA synthetase; Trps; angiogenesis; cytostatic;

KW Human; Rossmann fold nucleotide binding domain; chemokine; ENAM II;

KW vascular endothelial cell; solid tumour; myocardial infarction; enzyme;

KW endothelial monocyte-activating polypeptide II; tumour metastasis;

KW wound healing; dermal ulcer; endothelialisation; vascular graft surgery;

KW abdominal wound; coronary bypass surgery; gene therapy;

XX Homo sapiens.

OS Synthetic.

XX US200218266-A1.

PN US200218266-A1.

XX PD 05-DEC-2002.

XX PF 21-MAR-2001; 2001US-00813718.

XX FR 21-MAR-2001; 2001US-00813718.

YX (SCHMI /) SCHIMMEL P.

FA (WAKA /) WAKASUGI K.

YX SCHIMMEL P, Wakasugi K;

I1 WPI: 2003-340974/32.

I1 I.R. N-PSDB; ACA64106.

I1 New truncated tryptophanyl-tRNA synthetase polypeptide comprising a

I1 Rossmann fold nucleotide binding domain or having chemoattractant activity

I1 useful for e.g. for regulating angiogenesis and for treating myocardial

I1 infarction.

I1 Example 1; Page 46-47; 91pp; English.

I1 The invention relates to an isolated polypeptide comprising a truncated

CC tryptophanyl-tRNA synthetase (TrRS) polypeptide comprising a Rossmann

CC fold nucleotide binding domain or having chemokine activity. The isolated

CC polypeptide is capable of regulating vascular endothelial cell function;

CC C-terminal domain containing an ENAM II (endothelial monocyte

CC -activating polypeptide II, a proinflammatory cytokine)-like domain and

CC is similar in sequence to TrRS. Also included are a polynucleotide

CC encoding TrRS (or a polynucleotide 95% similar to it), a TrRS epitope,

CC 5' and 3' deletions of the TrRS polynucleotide, a recombinant vector

CC comprising an isolated TrRS nucleic acid, a recombinant host cell

CC TrRS antibody, producing truncations of TrRS by treating it with a

CC protease, and suppressing angiogenesis. Solid tumours or condition that

CC would benefit from decreased angiogenesis in a mammal by administering to

CC the mammal the composition comprising the TrRS truncated protein. The

CC isolated polypeptide is useful for the preparation of a pharmaceutical

CC composition for transdermal, transmucosal, enteral or parenteral

CC administration. The truncated tRNA synthetase polypeptide is useful for

CC research, diagnostic, prognostic and therapeutic applications. The tRNA

CC synthetase are useful for regulating vascular endothelial cell function,

CC particularly for regulating angiogenesis, for treating myocardial

CC infarction and solid tumour, and for suppressing tumour metastasis.

CC Angiogenic tRNA synthetase polypeptides are useful as dermal ulcers, in

CC the promotion of endothelialisation in vascular graft surgery, in the

CC treatment of abdominal wounds where there is a high risk infection, in
 CC conjunction with coronary bypass surgery by stimulating the growth of the
 CC transplanted tissue, and in gene therapy. The present sequence is a Trp
 CC tRNA synthetase protein (full length, truncated or mutant) with a His
 CC affinity tag
 XX SQ Sequence 437 AA;

Query Match 100.0%; Score 21116; DB 6; Length: 437;
 Best Local Similarity 100.0%; Pred. No. 1.e-202;
 Matches 401; Conservative 0; Missmatches 0; Indels 0; Gaps 0;

Qy	1 SNHGPDATTAEEEDFDPTPVQISSAKGIDYDKLIVRFGSSKIDELNIRATSGRPH 60
Db	24 SNHGPDATTAEEEDFDPTPVQISSAKGIDYDKLIVRFGSSKIDELNIRATSGRPH 83
Qy	61 FLERGIFFSHRDKNOVLDAYENKKPFLYLTGRGPSEAMHVGHLLIPFETKWLQDVNVVP 120
Db	84 FLERGIFFSHRDKNOVLDAYENKKPFLYLTGRGPSEAMHVGHLLIPFETKWLQDVNVVP 143
Qy	121 LVQMTDIBKYLMDLTQDAYDAVENAKDITACGFDTINKTFPFSDDYMGNSGFTK 180
Db	144 LVQMTDIBKYLMDLTQDAYDAVENAKDITACGFDTINKTFPFSDDYMGNSGFTK 202
Qy	181 VYRIQKHYTFKWKIGIFGFTSDPCIGKISFPALQAAFSNSPQIIFDRTDIQCILPCA 240
Db	204 VKIQRKHTFKYRGIFGFTSDPCIGKISFPALQAAFSNSPQIIFDRTDIQCILPCA 263
Qy	241 IDDPDPYFPMTRDVAAPRIGYPKPALLSTFPALQAGAQTKMSADDPNSSIFLDTAKQKT 300
Db	264 IDDPDPYFPMTRDVAAPRIGYPKPALLSTFPALQAGAQTKMSADDPNSSIFLDTAKQKT 323
Qy	301 KUNKHASSGGRTDIEHQFQGNCVDVSFMVDTFFLDDKLEQIRDYTSGAMLIGEL 360
Db	324 KUNKHASSGGRTDIEHQFQGNCVDVSFMVDTFFLDDKLEQIRDYTSGAMLIGEL 383
Qy	361 KHALIEVQPLIAHQARRKEYTDEIVKEFMMTPRKLSDFQ 401
Db	384 KHALIEVQPLIAHQARRKEYTDEIVKEFMMTPRKLSDFQ 424

RESULT 10

AB47615 standard; protein; 484 AA.

XX AC AAB47615;

XX DT 07-JAN-2002 (first entry)

XX DE Human full-length TrPRS.

XX Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain;
 XX vascular endothelial cell function; burn; plastic surgery; tumour metastasis;
 XX polymorphonuclear leucocyte elastase; angiogenesis; graft; myocardial infarction; solid tumour;
 XX dermal ulcer; diabetic ulcer; endothelialization; trypotophanyl-tRNA synthetase; tprrs; vascular graft surgery.

XX Homo sapiens.

XX AC AAB47615-A1.

XX DT 11-OCT-2001.

XX PN WO20017481-A1.

XX PR 21-MAR-2001; 2001WC-US00896.

XX PR 31-MAR-2003; 2000US-0193471P.

XX PA (SCRIPS RES INST.

XX PI Schimmel P, Wakasugi K;

XX DR WPI; 2001-526377/72.

DR	XX	TyRS; vascular endothelial cell function; angiogenesis; wound healing;
PT	XX	re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury;
PT	XX	diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction;
PT	XX	rheumatoid arthritis; vascular permeability;
XX	GS	psoriasis; diabetic retinopathy.
PS	PS	Homo sapiens.
XX	XX	W0200175078-A1.
CC	CC	PN
CC	CC	XX
CC	CC	PD 11-CCT-2001.
CC	CC	XX
CC	CC	PP 21-MAR-2001; 2001WO-US008975.
CC	CC	XX
CC	CC	PR 31-MAR-2000; 2000US-0193471P.
CC	CC	XX
CC	CC	(SCRI) SCRIPPS RES INST.
CC	CC	XX
CC	CC	Schimmel P, Wakasugi K,
CC	CC	XX
CC	CC	WPI: 2002-013784/01.
CC	CC	DR N-PSDB; ADD2448.
CC	CC	XX
CC	CC	Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in mammal.
CC	CC	XX
CC	CC	Example 1: Page 117-119; 149pp; English.
CC	CC	XX
CC	CC	The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrPRS) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to tyrosyl t-RNA synthetases (TyRS), TrPRS sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. Angiogenic TrRS sequences are useful as wound healing agents for revascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrPRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Angiogenic TrRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrPRS is also used in conjunction with angiography. TrPRS DNAs are useful in gene therapy. TrPRS antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenic activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrPRS by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rheumatoid arthritis, psoriasis, diabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human tryptophanyl t-RNA synthetase (TrPRS) in PET20B.
CC	CC	XX
CC	CC	Sequence 484 AA;
Q:	Q:	Sequence 484 AA;
DR:	DR:	Query Match 100.0%; Score 2116; DB 4; Length 484;
DR:	DR:	Best Local Similarity 100.0%; Pred. No. 1.4e-209;
DR:	DR:	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q:	Q:	1 SNHGDATEAEDFDPTWVQTSSAKGIDYDKL1TRFGSSKIDKELEINRERATGQRPHH 60
DR:	DR:	71 SNHGDATEAEDFDPTWVQTSSAKGIDYDKL1TRFGSSKIDKELEINRERATGQRPHH 130
Q:	Q:	61 FLRGIFFFSHRDMDNQVLDAYENIKKPFLYLYTGRGESEAMHYGHILFIFTKWLQDVENVYP 120
DR:	DR:	131 FLRGIFFFSHRDMDNQVLDAYENIKKPFLYLYTGRGESEAMHYGHILFIFTKWLQDVENVYP 190
Q:	Q:	121 LVQIMTDDEKYLWDKDLTDAYGDAVENAKDIIAGEDINXTF1FSDLDMGMSGFYKN 180
DR:	DR:	131 LVQIMTDDEKYLWDKDLTDAYGDAVENAKDIIAGEDINXTF1FSDLDMGMSGFYKN 250
Q:	Q:	181 VVKQKHTTNQVKGIFGFDSDCIGKISPAQSPFSENSPFQIPLRDTDICLIPCA 240
DR:	DR:	251 VVKQKHTTNQVKGIFGFDSDCIGKISPAQSPFSENSPFQIPLRDTDICLIPCA 310
Q:	Q:	241 IDQDPYFRMTRDVAPRIGYKPALKLHSTFPALQAGTQNSASPDNSSLFTDTAQIKT 300
DR:	DR:	311 IDQDPYFRMTRDVAPRIGYKPALKLHSTFPALQAGTQNSASPDNSSLFTDTAQIKT 370
Q:	Q:	301 KVNHAFSGSRDTTEHHQFGGNCDYDVSPMLTFPLEDDDKLQKRYDTSGAMLTGEL 360
DR:	DR:	371 KVNHAFSGSRDTTEHHQFGGNCDYDVSPMLTFPLEDDDKLQKRYDTSGAMLTGEL 430
Q:	Q:	361 KKALIEVQLPLIAHQARKEVTEIIVKEMTPKLISFDEQ 401
DR:	DR:	431 KKALIEVQLPLIAHQARKEVTEIIVKEMTPKLISFDEQ 471
Q:	Q:	Sequence Match 100.0%; Score 2116; DB 5; Length 484;
DR:	DR:	Best Local Similarity 100.0%; Pred. No. 1.4e-209;
DR:	DR:	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q:	Q:	1 SNHGDATEAEDFDPTWVQTSSAKGIDYDKL1TRFGSSKIDKELEINRERATGQRPHH 60
DR:	DR:	71 SNHGDATEAEDFDPTWVQTSSAKGIDYDKL1TRFGSSKIDKELEINRERATGQRPHH 130
Q:	Q:	61 FLRGIFFFSHRDMDNQVLDAYENIKKPFLYLYTGRGESEAMHYGHILFIFTKWLQDVENVYP 120
DR:	DR:	131 FLRGIFFFSHRDMDNQVLDAYENIKKPFLYLYTGRGESEAMHYGHILFIFTKWLQDVENVYP 190
Q:	Q:	121 LVQIMTDDEKYLWDKDLTDAYGDAVENAKDIIAGEDINXTF1FSDLDMGMSGFYKN 180

XX	OS	Homo sapiens.	Db	191	IVIQMTDDEKYLWKLDTLDQAYGDAVENAKDIIACGFDINKTPIFSDDYMGMSGFYKN 250
XX	Synthetic.		Qy	181	VVKIQKGVTFVQVKGIGFTSDCIGLSPQIAQAFSENSFPQIERTFRDIDQCLIPCA 240
XX	US2002182666-A1.		Db	251	VVKIQKGVTFVQVKGIGFTSDCIGLSPQIAQAFSENSFPQIERTFRDIDQCLIPCA 310
XX	05-DEC-2002.		Qy	241	IDQDPYERMTDVAPRIGYPKPALHSTFPALCGAQTMASDPNNSIFLTDTAKQIKT 300
XO	21-MAR-2001; 2001US-00813718.		Db	311	IDQDPYFRMTDVAPRIGYPKALLSTFFALQQQTMASDPNNSIFLTDTAKQIKT 370
XJ	21-MAR-2001; 2001US-00813718.		Qy	301	KVNKHAFSGGRDTTEHERQFGNCVDVSKYLTFLDEDKDKLEQRKDTSGANLTGEI 360
XJ	(SCHI/) SCHIMMEL, P.		Db	371	KVNKHAFSGGRDTTEHERQFGNCVDVSKYLTFLDEDKDKLEQRKDTSGANLTGEI 430
XJ	(WARA/) WAKASUGI, K.		Qy	361	KKALIEVLQPLIAEHQARRKTVTDELKEFMTPRKLSFDFQ 401
PJ	Schimmel, P., Wakasugi, K;		Db	431	KKALIEVLQPLIAEHQARRKTVTDELKEFMTPRKLSFDFQ 471
PI	WPI: 2003-340974/32.				
PI	N-PSDB: ACA64105.				
XX	New truncated triptophanyl-[tRNA synthetase polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity useful for e.g. for regulating angiogenesis and for treating myocardial infarction.				
PI	Example 1; Page 41-42; 91pp; English.				
PI	The invention relates to an isolated polypeptide comprising a truncated triptophanyl-tRNA synthetase (TrRS). Polypeptide comprising a Rossmann fold nucleotide binding domain or having chemokine activity. The isolated polypeptide is capable of regulating vascular endothelial cell function. TrRS has a C-terminal domain containing at: EMAP II (endothelial monocyte-activating polypeptide II), a proinflammatory cytokine-like domain and is similar in sequence to TrRS. Also included are a polynucleotide encoding TrRS (or a polynucleotide 95% similar to it) a TrRS epitope, 5', and 3', deletions of the TrRS polynucleotide, a recombinant vector comprising an isolated TrRS nucleic acid, a recombinant host cell containing the TrRS nucleic acid and expressing TrRS, an isolated anti-TrRS antibody, producing truncations of TrRS by treating it with a protease, and suppressing angiogenesis, solid tumours or a condition that would benefit from decreased angiogenesis in a mammal by administering to the mammal the composition comprising the TrRS truncated protein. The isolated polypeptide is useful for the preparation of a pharmaceutical composition for transmucosal, enteral or parenteral administration. The truncated tRNA synthetase polypeptide is useful for research, diagnostic, prognostic and therapeutic applications. The tRNA synthetase are useful for regulating angiogenesis, for treating myocardial infarction and solid tumour, and for suppressing tumour metastasis.				
CC	Angiogenic tRNA synthetase polypeptide are useful as wound healing agents or for treating full thickness wounds such as dermal ulcers in the promotion of endothelialisation in vascular graft surgery, in the treatment of abdominal wounds where there is a high risk infection, in conjunction with coronary bypass surgery by stimulating the growth of the transplanted tissue, and in gene therapy. The present sequence is a Trp tRNA synthetase protein (full length, truncated or mutant) with a His affinity tag				
CC	Sequence 4B4 AA:				
CC	Query Match 100.0%; Score 2116; DB 6; Length 484;				
CC	Best Local Similarity 100.0%; Pred. No. 1.4-e-209;				
CC	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Y	1 SNHGDPDATEAEEDFVDPTEVQSSAKGIDYDYLIVRGSSKIDKEELINIRETAGQPHH 60				
b	71 SNHGDPDATEAEEDFVDPTEVQSSAKGIDYDYLIVRGSSKIDKEELINIRETAGQPHH 130				
Y	61 FLRRGIFPFSHRMNQVLDAYENKPKFYXTGRGPSSAMHYCHLIPPIETFKLQDYNVP 120				
b	131 FLRRGIFPFSHRMNQVLDAYENKPKFYXTGRGPSSAMHYCHLIPPIETFKLQDYNVP 190				
Y	121 LVIQMTDDEKYLWKLDTLDQAYGDAVENAKDIIACGFDINKTPIFSDDYMGMSGFYKN 180				

(C identify a ligand which binds a polynucleotide. The library is chosen from DNA molecules, peptides, proteins and RNA molecules. The protein is useful for a high throughput screening of library of molecules or compounds to identify at least one ligand which specifically binds a protein, for purifying a ligand from a sample for making a antibody. The foam cell-expressed nucleic acids are useful for diagnosing cardiovascular disorder. The foam cell-expressed nucleic acids are useful as elements on a microarray which can be used for detecting related polynucleotide in a sample, diagnosing cardiovascular disease, atherosclerosis. The present sequence represents a protein differentially expressed in LPS treated foam cells.

(Q Sequence 471 AA;

Query Match 99.3%; Score 210; DB 7; Length 471;
Best Local Similarity 99.5%; Pred. No. 4.7e-208;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNRGDATEAEEFDYDPTWVOTSSARGIDYDYLIVRFGSSKIDKELEINRERATGPRHH 60

Db 71 SNHGDATEAEEFDYDPTWVOTSSARGIDYDYLIVRFGSSKIDKELEINRERATGPRHH 130

Qy 61 FLRRGIFFSHRMNQYLDAYENKEPELYTGRGPSSSEAMIVHLIPFIFTKWLQDYFNVP 120

Db 131 FLRRGIFFSHRMNQYLDAYENKEPELYTGRGPSSSEAMIVHLIPFIFTKWLQDYFNVP 190

Qy 121 LVQMTDDEKYLWQDYLQDAYGDAVENAKDIAQCDINKTFISLDDYNGMSSGFYK 180

Db 191 LVQMTDDEKYLWQDYLQDAYGDAVENAKDIAQCDINKTFISLDDYNGMSSGFYK 250

Qy 181 VVKIQLKHVTINQVKGIFGFTSDCGIKISPAIQAPSESNSPQIQRDTDIQCLIPCA 240

Db 251 VVKIQLKHVTINQVKGIFGFTSDCGIKISPAIQAPSESNSPQIQRDTDIQCLIPCA 310

Qy 241 IDQDPYFRMTRDVAIRGYKEPKALHSTTEPPALQAGQTMSASDENNSFLTDIAKQIKT 300

Db 311 IDQDPYFRMTRDVAIRGYKEPKALHSTTEPPALQAGQTMSASDENNSFLTDIAKQIKT 370

Qy 301 KVNRHAFSGGRDTIEHHRFGGNCVDYNSMILIEFELDDKKLBEIRKQYTSGAMLTGEL 360

Db 371 KVNRHAFSGGRDTIEHHRFGGNCVDYNSMILIEFELDDKKLBEIRKQYTSGAMLTGEL 430

Qy 361 KKLIELEVQPLIAHQARKEVTDIIVEKEMTPKLSFDFQ 401

Db 431 KKLIELEVQPLIAHQARKEVTDIIVEKEMTPKLSFDFQ 471

RESULT 15
ADE76998 standard; protein; 471 AA.

XX AC ADE76998;

XX DT 29-JAN-2004 (first entry)

XX DE Human protein expressed in a liver disorder #46.

XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder;

KW high-throughput screening; differential gene expression; gene therapy.

XX CS Homo sapiens.

XX IN US20031088771-A1.

XX 12-JUN-2003.

XX FR 30-JUL-2001; 2001US-C0919039.

XX FR 28-JUL-2000; 2000US-02222113P.

XX (KASE/1) KASSER M. R.

PI Kasser MR;

XX

DR WPI: 2004-031227/03.

DR N-PSDB; ADE76997.

XX

PT Compositon comprising several cDNAs that are differentially expressed in

PT treated human C3A liver cell cultures, useful for treating liver

PT disorders.

XX

PS Claim 1: SEQ ID NO 163; 41p; English.

XX

The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type

CC II diabetes, tumours of the liver and disorders of the high-throughput method

CC of screening several molecules or compounds to identify a ligand which

CC specifically binds a cDNA.

CC A Protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or

CC compounds to identify at least one ligand which specifically binds the

CC protein which involves combining the protein encoded by the cDNA with several molecules or compounds under conditions to allow specific

CC binding, and detecting specific binding between the protein and a

CC molecule or compound, therefore identifying a ligand which specifically

CC binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to

CC formulate prognosis and to design a treatment regimen and to monitor the

CC efficacy of treatment. The present sequence represents the amino acid

CC sequence of a protein encoded by a cDNA differentially expressed in a

CC liver disorder.

XX

Sequence 471 AA;

Query Match 99.3%; Score 2101; DB 8; Length 471;
Best Local Similarity 99.5%; Pred. No. 4.7e-208;
Matches 399; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SNHGDATEAEEFDYDPTWVOTSSARGIDYDYLIVRFGSSKIDKELEINRERATGPRHH 60

Db 71 SNHGDATEAEEFDYDPTWVOTSSARGIDYDYLIVRFGSSKIDKELEINRERATGPRHH 130

Qy 61 FLRRGIFFSHRMNQYLDAYENKEPELYTGRGPSSSEAMIVHLIPFIFTKWLQDYFNVP 120

Db 131 FLRRGIFFSHRMNQYLDAYENKEPELYTGRGPSSSEAMIVHLIPFIFTKWLQDYFNVP 190

Qy 121 LVQMTDDEKYLWQDYLQDAYGDAVENAKDIAQCDINKTFISLDDYNGMSSGFYK 180

Db 191 LVQMTDDEKYLWQDYLQDAYGDAVENAKDIAQCDINKTFISLDDYNGMSSGFYK 250

Qy 181 VVKIQLKHVTINQVKGIFGFTSDCGIKISPAIQAPSESNSPQIQRDTDIQCLIPCA 240

Db 251 VVKIQLKHVTINQVKGIFGFTSDCGIKISPAIQAPSESNSPQIQRDTDIQCLIPCA 310

Qy 241 IDQDPYFRMTRDVAIRGYKEPKALHSTTEPPALQAGQTMSASDENNSFLTDIAKQIKT 300

Db 311 IDQDPYFRMTRDVAIRGYKEPKALHSTTEPPALQAGQTMSASDENNSFLTDIAKQIKT 370

Qy 301 KVNRHAFSGGRDTIEHHRFGGNCVDYNSMILIEFELDDKKLBEIRKQYTSGAMLTGEL 360

Db 371 KVNRHAFSGGRDTIEHHRFGGNCVDYNSMILIEFELDDKKLBEIRKQYTSGAMLTGEL 430

Qy 361 KKLIELEVQPLIAHQARKEVTDIIVEKEMTPKLSFDFQ 401

Db 431 KKLIELEVQPLIAHQARKEVTDIIVEKEMTPKLSFDFQ 471

Search completed: August 24, 2004, 17:50:32
Job time : 130 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 18:01:04 ; Search time 125 Seconds

(without alignments)
 1008.130 Million cell updates/sec

Title: US-09-813-718-10 COPY_71_471

Perfect score: 2116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 3
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/1/pubpaas/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaas/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score : 9

Query No.: 1

Match Length DB ID

Description

US-10-080-839-13

Query Match

100.0%

Score 2116; DB 12;

Length 401;

Best Local Similarity

100.0%;

Pred. No. 3_5e-205;

Mismatches 0;

Indels 0;

Gaps 0;

Qy

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SNCGPDATAEEEFVDDPNTVQTSAGKGDYDKLIVRFSKIDKEILNIRATGQRPH

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Db

1

SNCGPDATAEEEFVDDPNTVQTSAGKGDYDKLIVRFSKIDKEILNIRATGQRPH

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Qy

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Db

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FRLGRGFFSHRDINQVLDAYENKPKFVLYTGRPSSEAMHVGHLIPFLFTKMLQDVENVP

120

Qy

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LVIQMDDDEKYLWDLTDQAYDAVENAKDITACGFDFINKTRIFSDLYMGMSGGFYKN

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Db

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Db

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Db

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FRLGRGFFSHRDINQVLDAYENKPKFVLYTGRPSSEAMHVGHLIPFLFTKMLQDVENVP

120

Db

1

RESULT 2
 Sequence 14, Application US/09/813,718
 Publication No. US200913718
 GENERAL INFORMATION:
 APPLICANT: Schimmele, Paul;
 APPLICANT: Wakasugi, Keisuke;
 TITLE OF INVENTION: Human Aminocetyl-tRNA Synthetase Useful For The Regulation of Angiogenesis
 CURRENT APPLICATION NUMBER: US/10/080,819
 CURRENT FILING DATE: 2002-02-22
 PRIORITY FILING DATE: 2001-03-21
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 415
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Cleavage Product T1 of recombinant human tRPRs
 US-10-080-813-5

Query Match 100.0%; Score 2116; DB 9; Length 415;
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QY 61 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 120
 Db 62 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 121

QY 121 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 180
 Db 122 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 181

Query Match 100.0%; Score 2116; DB 9; Length 415;
 Best Local Similarity 100.0%; Prod. No. 3.7e-205;
 Matches 401; Indels 0; Gaps 0;

QY 1 SNHGPDATAEAEEDVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELEINIRERATGCRPHI 60
 Db 2 SNHGPDATAEAEEDVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELEINIRERATGCRPHI 61

QY 61 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 120
 Db 62 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 121

QY 121 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 180
 Db 122 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 181

QY 181 VVKIQKHTFNOVKGIFGFTSDCIGKISPPAIQAPSSNSFQIIFRDTDIQCLIPCA 240
 Db 182 VVKIQKHTFNOVKGIFGFTSDCIGKISPPAIQAPSSNSFQIIFRDTDIQCLIPCA 241

QY 241 IDQDPYFRMTRDVAPRIGYPKPAHLHSTFPALQATMSASPDNSSIIFLTDAQIKIT 300
 Db 242 IDQDPYFRMTRDVAPRIGYPKPAHLHSTFPALQATMSASPDNSSIIFLTDAQIKIT 301

QY 301 KVNRHAFSGCRDTLEHHRGFGNCNDVSPMFYLFEDDDKLQEQRKDYSQGMLTGEL 360
 Db 302 KVNRHAFSGCRDTLEHHRGFGNCNDVSPMFYLFEDDDKLQEQRKDYSQGMLTGEL 361

QY 361 KKAIEVLOPLIAHQARKEVTEIVKFMTPKLSEFDQ 401
 Db 362 KKAIEVLOPLIAHQARKEVTEIVKFMTPKLSEFDQ 402

RESULT 3
 US-10-080-813-5
 Sequence 5, Application US/10/080,819
 Publication No. US200913718
 GENERAL INFORMATION:
 APPLICANT: Schimmele, Paul;
 APPLICANT: Friedlander, Martin;
 TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived Polypeptides Useful For The Regulation of Angiogenesis
 CURRENT APPLICATION NUMBER: US/10/080,819
 CURRENT FILING DATE: 2002-02-22
 PRIORITY FILING DATE: 2001-03-23
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 5
 LENGTH: 415
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Cleavage Product T1 of recombinant human tRPRs
 US-10-080-813-5

Query Match 100.0%; Score 2116; DB 12; Length 415;
 Best Local Similarity 100.0%; Prod. No. 3.7e-205;
 Matches 401; Indels 0; Gaps 0;

QY 1 SNHGPDATAEAEEDVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELEINIRERATGCRPHI 60
 Db 2 SNHGPDATAEAEEDVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELEINIRERATGCRPHI 61

QY 61 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 120
 Db 62 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 121

QY 121 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 180
 Db 122 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 181

Query Match 100.0%; Score 2116; DB 9; Length 415;
 Best Local Similarity 100.0%; Prod. No. 3.7e-205;
 Matches 401; Indels 0; Gaps 0;

QY 1 SNHGPDATAEAEEDVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELEINIRERATGCRPHI 60
 Db 2 SNHGPDATAEAEEDVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELEINIRERATGCRPHI 61

QY 61 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 120
 Db 62 FLRRGICFFSHRDANQVLDAVENKKEPYLYTGRGSSEAMNGHLIPFIFTKWLQDVENVY 121

QY 121 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 180
 Db 122 LVICMTDDEKYLWDLTDQDAYDVAENKARDIIAGFDINNKTFLSDLYMGMSGFYKN 181

QY 181 VVKIQKHTFNOVKGIFGFTSDCIGKISPPAIQAPSSNSFQIIFRDTDIQCLIPCA 240
 Db 182 VVKIQKHTFNOVKGIFGFTSDCIGKISPPAIQAPSSNSFQIIFRDTDIQCLIPCA 241

QY 241 IDQDPYFRMTRDVAPRIGYPKPAHLHSTFPALQATMSASPDNSSIIFLTDAQIKIT 300
 Db 242 IDQDPYFRMTRDVAPRIGYPKPAHLHSTFPALQATMSASPDNSSIIFLTDAQIKIT 301

QY 301 KVNRHAFSGCRDTLEHHRGFGNCNDVSPMFYLFEDDDKLQEQRKDYSQGMLTGEL 360
 Db 302 KVNRHAFSGCRDTLEHHRGFGNCNDVSPMFYLFEDDDKLQEQRKDYSQGMLTGEL 361

QY 361 KKAIEVLOPLIAHQARKEVTEIVKFMTPKLSEFDQ 401
 Db 362 KKAIEVLOPLIAHQARKEVTEIVKFMTPKLSEFDQ 402

RESULT 4
 US-10-240-532-14
 Sequence 14, Application US/10/240,532
 Publication No. US2004009163A1
 GENERAL INFORMATION:
 APPLICANT: Schimmele, Paul;
 APPLICANT: Wakasugi, Keisuke;
 TITLE OF INVENTION: Human Aminocetyl-tRNA Synthetase Polypeptides Useful For The Regulation of Angiogenesis
 CURRENT APPLICATION NUMBER: US/10/240,532
 CURRENT FILING DATE: 2002-09-30
 PRIORITY APPLICATION NUMBER: PCT/US01/08975
 PRIORITY APPLICATION NUMBER: 2002-03-21

PRIOR APPLICATION NUMBER: US 60/193,471
 PRIORITY: Application Number: 2000-03-31
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 PENTABURE:
 OTHER INFORMATION: Description of Artificial Sequence: Human
 US-10-240-52A-14

Query Match Score 100.0%; Length 415;
 Best Local Similarity 100.0%; Pred. No. 3.7e-205;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFDVDPWTVQTSAAKGIDYKLVFSSKIDKEELNTERATGQRPHH 60
 Db 2 SNHGPDATAEEDFDVDPWTVQTSAAKGIDYKLVFSSKIDKEELNTERATGQRPHH 61

Qy 61 FLRRGIFFSRHMNOVLLDAYENKKPFLTYGRPSSEAMHYGLIPFIFTKWLQDVENVYP 120
 Db 62 FLRRGIFFSRHMNOVLLDAYENKKPFLTYGRPSSEAMHYGLIPFIFTKWLQDVENVYP 121

Qy 121 LVIONTDEDKYLWKDLTLQDAYNAKDITACGFINKPTEFSDIDYMGMSGFYKN 180
 Db 122 LVIONTDEDKYLWKDLTLQDAYNAKDITACGFINKPTEFSDIDYMGMSGFYKN 181

Qy 181 LVIONTDEDKYLWKDLTLQDAYNAKDITACGFINKPTEFSDIDYMGMSGFYKN 182

Qy 181 VVQIKQXHTENQVKGTGGFTSDICIKISPPQIQLGQTKMSADPNSSIFLTDTAQIKT 300
 Db 182 VVQIKQXHTENQVKGTGGFTSDICIKISPPQIQLGQTKMSADPNSSIFLTDTAQIKT 301

Qy 301 VVQIKQXHTENQVKGTGGFTSDICIKISPPQIQLGQTKMSADPNSSIFLTDTAQIKT 302

Db 302 VVQIKQXHTENQVKGTGGFTSDICIKISPPQIQLGQTKMSADPNSSIFLTDTAQIKT 303

Qy 361 KKALIEVLQPLIAEHQARRKEYTDEIYKEFMPRKLSDFQ 401
 Db 362 KKALIEVLQPLIAEHQARRKEYTDEIYKEFMPRKLSDFQ 402

RESULT 6
 US-09-813-718-12
 Sequence 12, Application US/09813718
 Publication No. US2011B26662A1

GENERAL INFORMATION:
 APPLICANT: Schimmel, Paul
 ATTORNEY/AGENT: WAKASUGI, Keisuke
 TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
 THE REGULATION OF ANGIogenesis
 FILE REFERENCE: 00-2221
 CURRENT APPLICATION NUMBER: US/09/813.718
 CURRENT FILING DATE: 2001-03-21
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn ver. 2.0
 SEQ ID NO 12
 LENGTH: 437
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: human mini
 OTHER INFORMATION: TrPRs in PET20B
 US-09-813-718-12

Query Match Score 100.0%; Length 437;
 Best Local Similarity 100.0%; Pred. No. 4e-205;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFDVDPWTVQTSAAKGIDYKLVFSSKIDKEELNTERATGQRPHH 60
 Db 24 SNHGPDATAEEDFDVDPWTVQTSAAKGIDYKLVFSSKIDKEELNTERATGQRPHH 63

Qy 61 FLRRGIFFSRHMNOVLLDAYENKKPFLTYGRPSSEAMHYGLIPFIFTKWLQDVENVYP 120
 Db 84 FLRRGIFFSRHMNOVLLDAYENKKPFLTYGRPSSEAMHYGLIPFIFTKWLQDVENVYP 143

Qy 121 LVIONTDEDKYLWKDLTLQDAYNAKDITACGFINKPTEFSDIDYMGMSGFYKN 180
 Db 144 LVICMWDDEKYLWKDLTLQDAYNAKDITACGFINKPTEFSDIDYMGMSGFYKN 203

Qy 181 VVQIKQXHTENQVKGTGGFTSDICIKISPPQIQLGQTKMSADPNSSIFLTDTAQIKT 300

RESULT 8
US-10-240-532-12
Sequence 12, Application US/10440532
Publication No. US2004009163A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
FILE REFERENCE: TSR1 720..1
CURRENT APPLICATION NUMBER: US/10/240,532
CURRENT FILING DATE: 2002-09-30
PRIORITY APPLICATION NUMBER: PCT/US01/08975
PRIORITY APPLICATION NUMBER: PCT/US1-03-21
PRIORITY APPLICATION NUMBER: US 60/193,471
PRIORITY APPLICATION NUMBER: 2000-03-31
NUMBER OF SEQ ID NO: 58
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 12
LENGTH: 437
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human mini
OTHER INFORMATION: TrpRS in PET20B
US-10-240-532-12

Query Match 100.0%; Score 2116; DB 15; Length 437;
Best Local Similarity 100.0%; Pred. No. 4e-205;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGPDATAEEDFVDPWVQTSSAKGIDYDKLIVRFGSSKIDELINERATGORPH 60
Db 24 SNHGPDATAEEDFVDPWVQTSSAKGIDYDKLIVRFGSSKIDELINERATGORPH 60
Qy 61 FLRGIFFSHRDKNQVLDAYENKPKFLYTRGPSSSEAMHVGHLIPFKFTKNUQDVNPW 126
Db 84 FLRGIFFSHRDKNQVLDAYENKPKFLYTRGPSSSEAMHVGHLIPFKFTKNUQDVNPW 126
D:5 84 FLRGIFFSHRDKNQVLDAYENKPKFLYTRGPSSSEAMHVGHLIPFKFTKNUQDVNPW 143
Qy 121 LVQMTDDEKYLWKLDTI-DQAYSDAVENAKDIIACGPJINKTPFSD-DYMGMSGPYKN 180
Db 144 LVQMTDDEKYLWKLDTI-DQAYSDAVENAKDIIACGPJINKTEFSLDYMGMSGPYKN 203
Qy 181 VVKIQHNTFNQVKG1SFPTDCIGKSFPAQAASSNSPQIFRDTDQCLIPCA 240
Db 204 VVKIQHNTFNQVKG1SFPTDCIGKSFPAQAASSNSPQIFRDTDQCLIPCA 263
Qy 241 IDDPYFRMTRDVAPRIYKPKPAHLHSTFPALQAGQTKMSADPNSSFLTDTAKOIKT 300
Db 264 IDDPYFRMTRDVAPRIYKPKPAHLHSTFPALQAGQTKMSADPNSSFLTDTAKOIKT 323
Qy 301 KVNKAFFSGRDTIEHQQGNCVDVSYFMYLTFEEDDKLEQIRKDYTSGAMLTCGL 360
Db 324 KVNKAFFSGRDTIEHQQGNCVDVSYFMYLTFEEDDKLEQIRKDYTSGAMLTCGL 383
Qy 361 KKLALIEVLQPLTAEHQARRKEYTDIYKEFMPYPRKLSFDQ 401
Db 384 KKLALIEVLQPLTAEHQARRKEYTDIYKEFMPYPRKLSFDQ 424

RESULT 9
US-10-240-527-12
Sequence 12, Application US/10240527A
Publication No. US20040152075A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase
FILE REFERENCE: TSR1 720..2
CURRENT APPLICATION NUMBER: US/10/240,527A
CURRENT FILING DATE: 2002-09-30
PRIORITY APPLICATION NUMBER: PCT/US1/08966

PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 6/193,471
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human mini TprS in pET20B
; U_10-24C-527A-12

Query Match Score 2116; DB 16; Length 437;
Best Local Similarity 100.0%; Pred. No. 4e-205;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q' 1 SNHGPDATAEEDFVDPWTVQTSAAKGIYDKLIVRFGSSKIDKELINERATGPRPH 60
D> 24 SNHGPDATAEEDFVDPWTVQTSAAKGIYDKLIVRFGSSKIDKELINERATGPRPH 60
Qy 61 FLRRGIFFFSHRDNNQVLDAYENKKPFYLTYGRGPSEANHVGHILIPFIFTKWLQDVFNVP 120
Db 84 FLRRGIFFFSHRDNNQVLDAYENKKPFYLTYGRGPSEANHVGHILIPFIFTKWLQDVFNVP 143
Qy 121 LVQMTDDEKYLWDLTLDQAYDAVENAKDIAGFDINKTPIFSDLDMGMSGFYKN 180
Db 144 LVQMTDDEKYLWDLTLDQAYDAVENAKDIAGFDINKTPIFSDLDMGMSGFYKN 203
Qy 181 VVKIQRHVNCFYKIGI GFPDSDCIGKISPPAQAPSNSFPQI FRDRTDQCLIPA 240
Db 204 VVKIQRHVNCFYKIGI GFPDSDCIGKISPPAQAPSNSFPQI FRDRTDQCLIPA 263
Qy 241 IDQDPYFRMTRDVAIRGYPKPALLESTFPALOGAQTMASDPNNSFLTDTAKIQT 300
Db 264 IDQDPYFRMTRDVAIRGYPKPALLESTFPALOGAQTMASDPNNSFLTDTAKIQT 323
Qy 301 KVNHAFSGGRDTIEHROFGNCDDVFSMYLTFELEDDKKLQIRKDYTSGMLTGEI 360
Db 324 KVNHAFSGGRDTIEHROFGNCDDVFSMYLTFELEDDKKLQIRKDYTSGMLTGEI 383
Qy 361 KKALIEVQLIAHQARKEVTDIKEFMTPKLSFDFQ 401
Db 384 KKALIEVQLIAHQARKEVTDIKEFMTPKLSFDFQ 424

RESULT 10
US 10-126-467B-2
; Sequence 2, Application US/10126467B
; Publication No. US20030055797A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
; CURRENT APPLICATION NUMBER: US 10/126,467B
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/3284,980
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/513,895
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/384,869
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
U_10-126-467B-2

Query Match Score 2116; DB 14; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.5e-205;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNHGPDATAEEDFVDPWTVQTSAAKGIYDKLIVRFGSSKIDKELINERATGPRPH 60
Db 71 SNHGPDATAEEDFVDPWTVQTSAAKGIYDKLIVRFGSSKIDKELINERATGPRPH 130
Qy 61 FLRRGIFFFSHRDNNQVLDAYENKKPFYLTYGRGPSEANHVGHILIPFIFTKWLQDVFNVP 120
Db 131 FLRRGIFFFSHRDNNQVLDAYENKKPFYLTYGRGPSEANHVGHILIPFIFTKWLQDVFNVP 190
Db 191 LVQMTDDEKYLWDLTLDQAYDAVENAKDIAGFDINKTPIFSDLDMGMSGFYKN 250
Qy 121 LVQMTDDEKYLWDLTLDQAYDAVENAKDIAGFDINKTPIFSDLDMGMSGFYKN 180
Db 191 LVQMTDDEKYLWDLTLDQAYDAVENAKDIAGFDINKTPIFSDLDMGMSGFYKN 250
Qy 181 VVKIQRHVNCFYKIGI GFPDSDCIGKISPPAQAPSNSFPQI FRDRTDQCLIPA 240
Db 251 VVKIQRHVNCFYKIGI GFPDSDCIGKISPPAQAPSNSFPQI FRDRTDQCLIPA 310
Qy 241 IDQDPYFRMTRDVAIRGYPKPALLESTFPALOGAQTMASDPNNSFLTDTAKIQT 300
Db 311 IDQDPYFRMTRDVAIRGYPKPALLESTFPALOGAQTMASDPNNSFLTDTAKIQT 370
Qy 301 KVNHAFSGGRDTIEHROFGNCDDVFSMYLTFELEDDKKLQIRKDYTSGMLTGEI 360
Db 371 KVNHAFSGGRDTIEHROFGNCDDVFSMYLTFELEDDKKLQIRKDYTSGMLTGEI 430
Qy 361 KKALIEVQLIAHQARKEVTDIKEFMTPKLSFDFQ 401
Db 431 KKALIEVQLIAHQARKEVTDIKEFMTPKLSFDFQ 471

RESULT 11
US 10-295-027-1234
; Sequence 1.24, Application US/10295327
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: BioTechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; Methods of Screening for Modulators of Cancer
; CURRENT APPLICATION NUMBER: US 10/295,027
; PRIORITY FILING DATE: 2002-11-13
; PRIORITY APPLICATION NUMBER: 018501-012500US
; FILE REFERENCE: 018501-012500US
; PRIORITY FILING DATE: 2000-09-15
; PRIORITY APPLICATION NUMBER: US 09/663,733
; PRIORITY FILING DATE: 2001-11-13
; PRIORITY APPLICATION NUMBER: US 09/350,666
; PRIORITY FILING DATE: 2001-11-15
; PRIORITY APPLICATION NUMBER: US 09/335,394
; PRIORITY FILING DATE: 2001-11-21
; PRIORITY APPLICATION NUMBER: US 09/334,393
; PRIORITY FILING DATE: 2001-11-29
; PRIORITY APPLICATION NUMBER: US 09/340,376
; PRIORITY FILING DATE: 2001-12-14
; PRIORITY APPLICATION NUMBER: US 09/347,211
; PRIORITY FILING DATE: 2002-01-08
; PRIORITY APPLICATION NUMBER: US 09/347,349
; PRIORITY FILING DATE: 2002-01-10
; PRIORITY APPLICATION NUMBER: US 09/355,250
; PRIORITY FILING DATE: 2002-02-08
; PRIORITY APPLICATION NUMBER: US 09/356,714
; PRIORITY FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PAIR.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1234
LENGTH: 471
TYPE: PRT
ORGANISM: Homo sapiens
U-10-295-027-1234

Query Match 100.0%; Score 2116; DB 15; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.5e-205; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q: 1 SNHGPDATEAEEDFVDPWTVQTSAGKIDYDKLIVREGSSKIDKELEINERATGORPHH 60
Dl, 71 SNHGPDATEAEEDFVDPWTVQTSAGKIDYDKLIVREGSSKIDKELEINERATGORPHH 130

Qy 61 FLRGIFFFSHRDMMQVLDAENKPKLYTSGRGPSSAMHYGHLLIPITFKWLQDYFNVP 120
Db 131 FLRGIFFFSHRDMMQVLDAENKPKLYTSGRGPSSAMHYGHLLIPITFKWLQDYFNVP 190

Qy 121 LV1QMTDDEKYLWKLDTLDQAYDAVENAKDIIACGPDINKTIFSDIDYGMSSGFYKN 180
Db 191 LV1QMTDDEKYLWKLDTLDQAYDAVENAKDIIACGPDINKTIFSDIDYGMSSGFYKN 250

Qy 181 VVKIQKHTENQVKCIGFTOSDCIGKISFPQLFRCPDIOCLPCA 240
Db 251 VVKIQKHTENQVKCIGFTOSDCIGKISFPQLFRCPDIOCLPCA 310

Qy 241 IDQDPYRMTDVAPIGYKPALLHSTFPALQGAQTKMSADPNSSIFLTDTAQIKT 300
Db 311 IDQDPYRMTDVAPIGYKPALLHSTFPALQGAQTKMSADPNSSIFLTDTAQIKT 370

Qy 301 KVNKAFASSGRDTIEERQFGNCYDVSFMYLTFFLEDKLEQIRKDYISSGMLTGEL 360
Db 371 KVNKAFASSGRDTIEERQFGNCYDVSFMYLTFFLEDKLEQIRKDYISSGMLTGEL 430

Db 431 KRALIEVQPLIAHQARRKEYDIEVKEFMPRKLSFDFQ 471

RESULT 13
US-10-080-839-1
; Sequence 1, Application US/10080839
; Publication No. US2003001756A1
GENERAL INFORMATION:
; APPLICANT: Schimmele, Paul
; APPLICANT: Wakanugi, Keisuke
; APPLICANT: Friedlander, Martin
TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived Polypeptides Useful For The Regulation of Argogenesis
FILE REFERENCE: TSRI-813-1
CURRENT APPLICATION NUMBER: US/10080839
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/270,951
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 484
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Recombinant human trprs
US-10-080-839-1

Query Match 100.0%; Score 2116; DB 12; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.7e-205;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGDATEAEEDFVDPWTVQTSAGKIDYDKLIVREGSSKIDKELEINERATGORPHH 60
Db 71 SNHGDATEAEEDFVDPWTVQTSAGKIDYDKLIVREGSSKIDKELEINERATGORPHH 130

Qy 61 FLRRGIFFFSHRDMMQVLDAENKPKLYTSGRGPSSAMHYGHLLIPITFKWLQDVNVP 190
Db 131 FLRRGIFFFSHRDMMQVLDAENKPKLYTSGRGPSSAMHYGHLLIPITFKWLQDVNVP 250

Qy 121 LV1QMTDDEKYLWKLDTLDQAYDAVENAKDIIACGPDINKTIFSDIDYGMSSGFYKN 180
Db 191 LV1QMTDDEKYLWKLDTLDQAYDAVENAKDIIACGPDINKTIFSDIDYGMSSGFYKN 250

Query Match 100.0%; Score 2116; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 4.7e-205; Indels 0; Gaps 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNHGDATEAEEDFVDPWTVQTSAGKIDYDKLIVREGSSKIDKELEINERATGORPHH 60
Db 71 SNHGDATEAEEDFVDPWTVQTSAGKIDYDKLIVREGSSKIDKELEINERATGORPHH 130

Qy 61 FLRRGIFFFSHRDMMQVLDAENKPKLYTSGRGPSSAMHYGHLLIPITFKWLQDVNVP 120
Db 131 FLRRGIFFFSHRDMMQVLDAENKPKLYTSGRGPSSAMHYGHLLIPITFKWLQDVNVP 190

Qy 301 KVNKAFASSGRDTIEERQFGNCYDVSFMYLTFFLEDKLEQIRKDYISSGMLTGEL 360

RESULT 14
 US-10-240-532-10
 ; Sequence 10, Application US/10240532
 ; Publication No. US2004009163A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schimmel, Paul
 ; TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For Regulation of Angiogenesis
 ; FILE REFERENCE: TSP1 720.1
 ; CURRENT APPLICATION NUMBER: US/10/240,532
 ; CURRENT FILING DATE: 2002-09-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/08975
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US/60/193,471
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 10
 ; LENGTH: 484
 ; TYPE: PTM
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: human
 ; OTHER INFORMATION: Full-length TrPRs in PET20B
 ; US-10-240-532-10

Query Match Score 2116; DB 15; Length 484;
 Best Local Similarity 100.0%; Pred. No. 4.7e-205;
 Mismatches 0; Indels 0; Gaps 0;

CY 1 SNHGDATATEEDFDVDPWIVQTSAKGDIDKLYREGSSKIDKELINRTERATGQRPH 60
 CY 1 SNHGDATATEEDFDVDPWIVQTSAKGDIDKLYREGSSKIDKELINRTERATGQRPH 60
 DB 71 SNHGDATATEEDFDVDPWIVQTSAKGDIDKLYREGSSKIDKELINRTERATGQRPH 130
 DB 71 SNHGDATATEEDFDVDPWIVQTSAKGDIDKLYREGSSKIDKELINRTERATGQRPH 130
 CY 61 FLRRGIFFSHRDMNCVLDAVENKEPFYLYTGRGPSEAMEVGHILPFFKWLQDVFNVP 120
 CY 61 FLRRGIFFSHRDMNCVLDAVENKEPFYLYTGRGPSEAMEVGHILPFFKWLQDVFNVP 120
 DB 131 FLRRGIFFSHRDMNCVLDAVENKEPFYLYTGRGPSEAMEVGHILPFFKWLQDVFNVP 190
 DB 131 FLRRGIFFSHRDMNCVLDAVENKEPFYLYTGRGPSEAMEVGHILPFFKWLQDVFNVP 190
 CY 121 LVIQMTDDEKVWKLQDLYGDAVENAKDILAGCFEINKTFIFSDLDNGMSSGFYKN 180
 CY 121 LVIQMTDDEKVWKLQDLYGDAVENAKDILAGCFEINKTFIFSDLDNGMSSGFYKN 180
 DB 191 LVIQMTDDEKVWKLQDLYGDAVENAKDILAGCFEINKTFIFSDLDNGMSSGFYKN 250
 DB 191 LVIQMTDDEKVWKLQDLYGDAVENAKDILAGCFEINKTFIFSDLDNGMSSGFYKN 250
 CY 181 VVKIQKHTENQVKCIGFTSDCIGKISPAIQOAPSFSNSFQPLFRDIDQCLIPCA 240
 CY 181 VVKIQKHTENQVKCIGFTSDCIGKISPAIQOAPSFSNSFQPLFRDIDQCLIPCA 240
 DB 251 VVKIQKHTENQVKCIGFTSDCIGKISPAIQOAPSFSNSFQPLFRDIDQCLIPCA 320
 DB 251 VVKIQKHTENQVKCIGFTSDCIGKISPAIQOAPSFSNSFQPLFRDIDQCLIPCA 320
 CY 241 IDQDPYFRMTEDVAPRIGYPKALIISTFPALQGQTRNSASDPNSIPLTDQKIKT 300
 CY 241 IDQDPYFRMTEDVAPRIGYPKALIISTFPALQGQTRNSASDPNSIPLTDQKIKT 300
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 DB 311 IDQDPYFRMTEDVAPRIGYPKALIISTFPALQGQTRNSASDPNSIPLTDQKIKT 370
 CY 301 KUNKHAFSGGDDCTIEHROFGNCNDVDSFMYLTFFILEDDDKLEQIRKDYSGAMLTGEL 360
 CY 301 KUNKHAFSGGDDCTIEHROFGNCNDVDSFMYLTFFILEDDDKLEQIRKDYSGAMLTGEL 360
 DB 371 KUNKHAFSGGDDCTIEHROFGNCNDVDSFMYLTFFILEDDDKLEQIRKDYSGAMLTGEL 430
 DB 371 KUNKHAFSGGDDCTIEHROFGNCNDVDSFMYLTFFILEDDDKLEQIRKDYSGAMLTGEL 430
 CY 361 KKALIEVQPLIAEFQARRKEYDEIYKEFMPRKLSFDFQ 401
 CY 361 KKALIEVQPLIAEFQARRKEYDEIYKEFMPRKLSFDFQ 401
 DB 431 KKALIEVQPLIAEFQARRKEYDEIYKEFMPRKLSFDFQ 471
 DB 431 KKALIEVQPLIAEFQARRKEYDEIYKEFMPRKLSFDFQ 471

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